

GenCore version 5.1.3
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OW protein - protein search, using sw model

Run on: January 7, 2003, 17:12:13 ; Search time 15 Seconds
(without alignments)
70.499 Million cell updates/sec

Title: US-09-623-006b-5
Perfect score: 57
Sequence: 1 MKRQLTPYIQR 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR-F3:
2: PIR-F3:
3: PIR-F3:
4: PIR-F3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	57	100.0	391 1 LPRTA4	apolipoprotein A-I
2	50	87.7	391 2 B40892	apolipoprotein A-I
3	50	87.7	394 2 A25281	apolipoprotein A-I
4	50	87.7	395 2 A40882	apolipoprotein A-I
5	50	87.7	399 2 C40892	apolipoprotein A-I
6	46	80.7	401 2 A47141	apolipoprotein A-I
7	46	80.7	429 2 S29565	apolipoprotein A-I
8	41	71.9	308 2 AH1898	apolipoprotein A-I
9	41	71.9	352 1 BVECHD	permease protein c
10	41	71.9	352 2 A90728	apolipoprotein A-I
11	41	71.9	352 2 AE0595	AMP-binding compo
12	41	71.9	352 2 B85579	molypdenum transpo
13	40	70.2	242 2 T20976	ATP-binding compo
14	39	68.4	476 1 VYRTD	hypothetical prote
15	38	66.7	359 2 A10140	vitamin D-binding
16	38	66.7	641 2 S23757	molypdenum transpo
17	38	66.7	657 1 I40188	reticacycline resis
18	37	64.9	224 2 AC3627	maltose/maltodextr
19	37	64.9	342 2 AD2867	hypothetical prote
20	37	64.9	342 2 G98315	thunk protein (AF17
21	37	64.9	342 2 B95881	probable trehalose
22	37	64.9	515 2 G72097	hypothetical prote
23	37	64.9	515 2 E86526	hypothetical prote
24	36	63.2	246 2 F72769	hypothetical prote
25	36	63.2	472 1 A35327	vitamin D-binding
26	36	63.2	640 2 F83303	threonyl-cRNA synt
27	36	63.2	911 2 JC6016	chitin synthase (E
28	36	63.2	916 2 JC2315	chitin synthase (E
29	35	61.4	184 2 B84259	hypothetical prote

30	35	61.4	300 2 A69351	heterodisulfide re
31	35	61.4	321 2 E81725	Mes/Ycf62 family
32	35	61.4	348 2 E70009	conserved hypoten
33	35	61.4	1058 2 UC1254	ubiquitin-protein
34	35	61.4	1661 2 S64800	probable membrane
35	35	61.4	1747 2 A54121	collagen alpha-4 c
36	34	59.6	102 2 A24846	apolipoprotein A-I
37	34	59.6	172 2 T13203	probable terminase
38	34	59.6	177 2 T16280	hypothetical prote
39	34	59.6	289 2 A13166	hypothetical prote
40	34	59.6	318 2 AD3200	conserved hypoten
41	34	59.6	366 2 I38888	mannitol-1-phospha
42	34	59.6	368 2 C90011	mannitol-1-phospha
43	34	59.6	374 2 C84131	PTS system, mannit
44	34	59.6	419 2 T19260	hypothetical prote
45	34	59.6	642 2 AB0297	threonine-cRNA lig

ALIGNMENTS

RESULT 1

LPRTA4

apolipoprotein A-IV precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 27-Nov-1985 #sequence revision 27-Nov-1985 #text_change 22-Jun-1999

C:Accession: A03095; A25214; G24700

R:Boyski, M.S.; Elshourbagy, N.A.; Taylor, J.M.; Gordon, J.I.

Proc. Natl. Acad. Sci. U.S.A. 81, 5021-5025, 1984

A:Title: Rat apolipoprotein A-IV contains 13 tandem repetitions of a 22-amino acid segmen

A:Reference number: A03095; NCID:84298074; PMID:6591177

A:Accession: A03095

A:Molecule type: mRNA

A:Residues: 1-391 <BOG>

A:Cross-references: GB:M00002; GB:K02421; NID:G202949; PIDN:AAA85909.1; PID:G202950

R:Boyski, M.S.; Birkemeier, E.H.; Elshourbagy, N.A.; Taylor, J.M.; Gordon, J.I.

J. Biol. Chem. 261, 6398-6407, 1986

A:Title: Evolution of the apolipoproteins. Structure of the rat APO-A-IV gene and its re

A:Reference number: A25214; NCID:86196059; PMID:3009456

A:Accession: A25214

A:Molecule type: protein

A:Residues: 1-252, 'Q', 254-391 <BO2>

R:Hadad, I.A.; Ordovas, J.M.; Fitzpatrick, T.; Karathanasis, S.K.

J. Biol. Chem. 261, 13268-13277, 1986

A:Title: Linkage, evolution, and expression of the rat apolipoprotein A-I, C-III, and A-I

A:Reference number: A92558; NCID:87008540; PMID:3020028

A:Accession: C24700

A:Molecule type: DNA

A:Residues: 1-252, 'Q', 254-391 <HAD>

A:Cross-references: GB:J02588; NID:G202937; PIDN:AAA40747.1; PID:G202941

C:Comment: This apoprotein is a major component of HDL and chylomicrons but, unlike other

C:Comment: Nine of the thirteen 22-amino acid tandem repeats (each 22-mer is actually a t

cal, and many of these helices are amphipathic. They may therefore serve as lipid-binding

C:Keywords: chylomicron; duplication; HDL; lipid transport; plasma; tandem repeat

F:1-20/Domain: signal sequence #status predicted <SIS>

F:21-91/Product: apolipoprotein A-IV #status predicted <MAT>

F:33-330/Region: 22-residue repeats

Query Match 100.0%; Score 57; DB 1; Length 391;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRQLTPYIQR 11
DB 153 MKRQLTPYIQR 163

RESULT 2

B40892

apolipoprotein A-IV precursor - mouse (strain 129)

C:Species: Mus musculus (house mouse)

C:Date: 27-Mar-1992 #sequence revision 10-Apr-1992 #text_change 13-Aug-1999

C;Accession: B40892
R;Reue, K.; Leete, T.H.
J. Biol. Chem. 266, 12715-12721, 1991
A;Title: Genetic variation in mouse apolipoprotein A-IV due to insertion and deletion in
A;Reference number: A40892; MUID:91286309; PMID:1648102
A;Accession: B40892
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-391 <REU>
A;Cross-references: GB:M64248; NID:g191884; PIDN:AAA37214.1; PID:g191885
A;Note: the authors translated the codon CTG for residue 87 as Glu, GAG for residue 207
C;Superfamily: apolipoprotein A-I
C;Keywords: lipid binding; lipoprotein

Query Match 87.7%; Score 50; DB 2; Length 391;
Best Local Similarity 90.9%; Pred. No. 0.073;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRLQTPYIQR 11
||| |||||
Db 153 MKLQTPYIQR 163

RESULT 3
A25281
apolipoprotein A-IV precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 13-Aug-1999
C;Accession: A25281
R;Williams, S.C.; Bruckheimer, S.M.; Lusis, A.J.; LeBoeuf, R.C.; Kinniburgh, A.J.
Mol. Cell. Biol. 6, 3807-3814, 1986
A;Title: Mouse apolipoprotein A-IV gene: nucleotide sequence and induction by a high-lip
A;Reference number: A25281; MUID:87089722; PMID:3796595
A;Accession: A25281
A;Molecule type: DNA
A;Residues: 1-394 <WIL>
A;Cross-references: GB:M13966; NID:g192006; PIDN:AAA37253.1; PID:g387102
C;Genetics:
A;Introns: 16/1, 58/2
C;Superfamily: apolipoprotein A-I
C;Keywords: chylomicron; HDL; lipid binding; lipoprotein

Query Match 87.7%; Score 50; DB 2; Length 394;
Best Local Similarity 90.9%; Pred. No. 0.074;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRLQTPYIQR 11
||| |||||
Db 152 MKLQTPYIQR 162

RESULT 4
A40892
apolipoprotein A-IV precursor - mouse (strain C57BL/16)
C;Species: Mus musculus (house mouse)
C;Date: 27-Mar-1992 #sequence_revision 10-Apr-1992 #text_change 13-Aug-1999
C;Accession: A40892
R;Reue, K.; Leete, T.H.
J. Biol. Chem. 266, 12715-12721, 1991
A;Title: Genetic variation in mouse apolipoprotein A-IV due to insertion and deletion in
A;Reference number: A40892; MUID:91286309; PMID:1648102
A;Accession: A40892
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-395 <REU>
A;Cross-references: GB:M64249; NID:g191886; PIDN:AAA37215.1; PID:g191887
A;Note: the authors translated the codon CTG for residue 87 as Glu, GAG for residue 207
C;Superfamily: apolipoprotein A-I
C;Keywords: lipid binding; lipoprotein

Query Match 87.7%; Score 50; DB 2; Length 395;
Best Local Similarity 90.9%; Pred. No. 0.074;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRLQTPYIQR 11
||| |||||
Db 153 MKLQTPYIQR 163

RESULT 5 C40892

apolipoprotein A-IV precursor - mouse
C;Species: Mus musculus castaneus (southeastern Asian house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 31-Dec-1993
C;Accession: C40892
R;Reue, K.; Leete, T.H.
J. Biol. Chem. 266, 12715-12721, 1991
A;Title: Genetic variation in mouse apolipoprotein A-IV due to insertion and deletion in
A;Reference number: A40892; MUID:91286309; PMID:1648102
A;Accession: C40892
A;Molecule type: mRNA
A;Residues: 1-399 <REU>
A;Cross-references: GB:M64250
A;Note: the authors translated the codon CTG for residue 87 as Glu, GAG for residue 207
C;Superfamily: apolipoprotein A-I
C;Keywords: chylomicron; duplication; HDL; lipid binding; lipid transport; lipoprotein;

Query Match 87.7%; Score 50; DB 2; Length 399;
Best Local Similarity 90.9%; Pred. No. 0.075;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRLQTPYIQR 11
||| |||||
Db 153 MKLQTPYIQR 163

RESULT 6 A47141

apolipoprotein A-IV I isoform - baboon (fragment)
C;Species: Papio sp. (baboon)
C;Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 12-Apr-1995
C;Accession: A47141
R;Hixson, J.E.; Kammerer, C.M.; Mott, G.E.; Britten, M.L.; Birnbaum, S.; Powers, P.K.;
J. Biol. Chem. 268, 15667-15673, 1993
A;Title: Baboon apolipoprotein A-IV. Identification of Lys76-->Glu that distinguishes t
A;Reference number: A47141; MUID:93340170; PMID:8101842
A;Accession: A47141
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-401 <HIX>
A;Experimental source: intestine
A;Note: sequence extracted from NCBI backbone (NCBIN:136009, NCBIP:136010)
C;Superfamily: apolipoprotein A-I

Query Match 80.7%; Score 46; DB 2; Length 401;
Best Local Similarity 72.7%; Pred. No. 0.45;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRLQTPYIQR 11
.:||| |||||
Db 137 LRRQLTPYIQR 147

RESULT 7 S29565

apolipoprotein A-IV - crab-eating macaque
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 13-Aug-1999
C;Accession: S30195; S29565
R;Osada, J.; Pocovi, M.; Nicolosi, R.J.; Schaefer, E.J.; Ordovas, J.M.
Biochim. Biophys. Acta 1172, 335-339, 1993
A;Title: Nucleotide sequences of the Macaca fascicularis apolipoprotein C-III and A-IV
A;Reference number: S30195; MUID:93192330; PMID:8448212
A;Accession: S30195
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-429 <OSA>
A;Cross-references: EMBL:X68361, NID:G38050; PIDN:CAA48421.1; PID:G38051
C;Genetics:
A;Introns: 17/1; 59/2
C;Superfamily: apolipoprotein A-I

Query Match 80.7%; Score 46; DB 2; Length 429;
Best Local Similarity 72.7%; Pred. No. 0.48;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKRQLTPYIQR 11
Db 153 LRRQLTPYIAQR 163

RESULT 8

AH1898
permease protein of sugar ABC transporter alr0738 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp.
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Accession: AH1898
R;Kaneko, T.; Nakamura, Y.; Molk, C.P.; Kunitz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AH1898
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1308 <KTR>
A;Cross-references: GB:BA000019; PIDN:BAE72695.1; PID:G17130083; GSPDB:GN00179.
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr0738
C;Superfamily: inner membrane protein ugpa

Query Match 71.9%; Score 41; DB 2; Length 308;
Best Local Similarity 77.8%; Pred. No. 3.2;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKRQLTPYI 9
Db 12 IKRQLTPYI 20

RESULT 9

BYE6HD
molybdenum transport protein modC - Escherichia coli (strain K-12)
N;Alternate names: molybdenum transport protein chlD
C;Species: Escherichia coli
C;Date: 31-Dec-1990 #sequence_revision 31-Oct-1997 #text_change 19-Jul-2002
R;Baltner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
C;Accession: E64812
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-352 <BLAT>
A;Cross-references: GB:AE000179; GB:U00096; NID:G1786978; PIDN:AACT3852.1; PID:G1786981;
A;Experimental source: strain K-12, Substrain MG1655
R;Johann, S.; Hinton, S.M.
J. Bacteriol. 169, 1911-1916, 1987
A;Title: Cloning and nucleotide sequence of the chlD locus.
A;Reference number: A26871; MUID:87194564; PMID:3553151
A;Accession: B26871
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-243, 'SALRDDR', 251-268, 'LRYVPHSGFRCFSPFNRRSKP', 269, 'EVT', 273, 'AGKSC', <JOH>
A;Cross-references: EMBL:X07875
A;Experimental source: strain K12

A;Note: the authors translated the codon GAA for residue 74 as Gly

C;Genetics:
A;Gene: modC; chlD
A;Map position: 17 min

C;Function:
A;Description: nucleotide-binding protein component of the binding protein-dependent transport system
C;Superfamily: molybdenum transport protein modC; ATP-binding cassette homology
C;Keywords: ATP; inner membrane; molybdenum transport; nucleotide binding; P-loop
F;14-205/Domain: ATP-binding cassette homology <ABC>
F;31-38/Region: nucleotide-binding motif A (P-loop)
F;149-153/Region: nucleotide-binding motif B

Query Match 71.9%; Score 41; DB 1; Length 352;
Best Local Similarity 70.0%; Pred. No. 3.7;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KRQLTPYIQR 11
Db 164 KRELTPYIQR 173

RESULT 10

A90728
ATP-binding component of molybdate transport [imported] - Escherichia coli (strain O157:H7)
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 19-Jul-2002
C;Accession: A90728
R;Hayashi, T.; Makino, K.; Ohishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.; Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genome
A;Reference number: A9629; MUID:21156231; PMID:11258796
A;Accession: A90728
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-352 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAE34216.1; PID:G1336025; GSPDB:GN00154
A;Experimental source: strain O157:H7, Substrain R1MD 0509952
C;Genetics:
A;Gene: BCS0793
C;Superfamily: molybdenum transport protein modC; ATP-binding cassette homology

Query Match 71.9%; Score 41; DB 2; Length 352;
Best Local Similarity 70.0%; Pred. No. 3.7;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KRQLTPYIQR 11
Db 164 KRELTPYIQR 173

RESULT 11

AE0595
molybdenum transport ATP-binding protein ModC STY0816 [imported] - Salmonella enterica serovar Typhimurium
C;Species: Salmonella enterica subsp. enterica serovar Typhimurium
A;Note: This species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 19-Jul-2002
C;Accession: AE0595
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, J.; Moule, S.; O'Garra, P.
Nature 413, 848-852, 2001
A;Authors: Farrar, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhimurium
A;Reference number: AB0502; PMID:11677608
A;Accession: AE0595
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-352 <PAR>
A;Cross-references: GB:AL513382; PIDN:CA005231.1; PID:G16502001; GSPDB:GN00176
C;Genetics:
A;Gene: STY0816
C;Superfamily: molybdenum transport protein modC; ATP-binding cassette homology

Query Match 71.9%; Score 41; DB 2; Length 352;
 Best Local Similarity 70.0%; Pred. No. 3.7;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KRQLTPYIQR 11
 |||:|:|:|
 DB 164 KRELLPYLQR 173

RESULT 12
 B85579
 ATP-binding component of molybdate transport [imported] - Escherichia coli (strain O157:
 C:Species: Escherichia coli
 C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 19-Jul-2002
 C:Accession: B85579
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaesner, J.D.; Rose, D.J.; Mayhew
 iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouasis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: B85579
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-352 <STO>
 A:Cross-references: GB:AE005174; NID:gl2513697; PIDN:AAG55094.1; GSPDB:GN00145; UMG:P:Z09
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: modC
 C:Superfamily: molybdenum transport protein modC; ATP-binding cassette homology

Query Match 71.9%; Score 41; DB 2; Length 352;
 Best Local Similarity 70.0%; Pred. No. 3.7;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KRQLTPYIQR 11
 |||:|:|:|
 DB 164 KRELLPYLQR 173

RESULT 13
 T20976
 hypothetical protein F15D3.7 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T20976
 R:White, S.
 submitted to the EMBL Data Library, October 1996
 A:Reference number: Z19353
 A:Accession: T20976
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-242 <WTL>
 A:Cross-references: EMBL:Z81063; PIDN:CAB02956.1; GSPDB:GN00019; CESP:F15D3.7
 A:Experimental source: clone F15D3
 C:Genetics:
 A:Gene: CESP:F15D3.7
 A:Map position: 1
 A:Introns: 42/3; 114/2

Query Match 70.2%; Score 40; DB 2; Length 242;
 Best Local Similarity 60.0%; Pred. No. 3.9;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRQLTPYIQ 10
 :||:|:|:|
 DB 71 VSRQMTPTYVQ 80

RESULT 14
 VYRTD
 vitamin D-binding protein precursor - rat
 N:Alternate names: DBP; Gc-globulin; group-specific component

C:Species: Rattus norvegicus (Norway rat)
 C>Date: 04-Dec-1986 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
 C:Accession: A38726; A34161; A92576; A93050; A03238
 R:Ray, K.; Wang, X.; Zhao, M.; Cooke, N.E.
 J. Biol. Chem. 266, 6221-6229, 1991
 A:Title: The rat vitamin D binding protein (Gc-globulin) gene. Structural analysis, fun
 A:Reference number: A38726; MUID:91177870; PMID:2007578
 A:Accession: A38726
 A:Molecule type: DNA
 A:Residues: 1-476 <RAY>
 A:Cross-references: GB:M60197
 A:Experimental source: liver
 A>Note: the authors translated the codon CAG for residue 129 as Gly, CTT for residue 17.
 R:McLeod, J.F.; Cooke, N.E.
 J. Biol. Chem. 266, 21760-21769, 1989
 A:Title: The vitamin D-binding protein, alpha-fetoprotein, albumin multigene family: dei
 A:Reference number: A34161; MUID:90094352; PMID:2480956
 A:Accession: A34161
 A:Molecule type: mRNA
 A:Residues: 1-131, 'Q', 133-476 <MCL>
 A:Cross-references: GB:J05148; NID:G203940; PIDN:AAA41082.1; PID:G203941
 A:Experimental source: kidney
 R:Cooke, N.E.
 J. Biol. Chem. 261, 3441-3450, 1986
 A:Title: Rat vitamin D binding protein. Determination of the full-length primary struct
 A:Reference number: A92576; MUID:86140127; PMID:2419332
 A:Accession: A92576
 A:Molecule type: mRNA
 A:Residues: 1-173, 'P', 175-209, 'L', 211-476 <COO>
 A:Cross-references: GB:M12450; NID:G203926; PIDN:AAA41080.1; PID:G203927
 A:Experimental source: liver
 R:Litwiler, R.; Faser, D.; Kumar, R.
 Life Sci. 38, 2179-2184, 1986
 A:Title: The amino acid sequence of the NH-2-terminal portion of rat and human vitamin
 A:Reference number: A93050; MUID:86229807; PMID:3713442
 A:Accession: A93050
 A:Molecule type: protein
 A:Residues: 17-40 <LIT>
 C:Comment: DBP is a multifunctional protein found in plasma, ascitic fluid, cerebrospini
 nts polymerization of actin by binding its monomers. DBP associates with membrane-bound
 C:Genetics:
 A:Introns: 20/1; 43/2; 87/3; 158/2; 202/3; 234/2; 277/3; 345/2; 388/3; 421/2; 465/3
 C:Superfamily: serum albumin; serum albumin repeat homology
 C:Keywords: actin binding; duplication; globulin; glycoprotein; liver; plasma; polymorpi
 F:1-16/Domain: signal sequence #status predicted <SIG>
 F:17-476/Product: vitamin D-binding protein #status experimental <MPT>
 F:26-199/Domain: serum albumin repeat homology <SA1>
 F:217-385/Domain: serum albumin repeat homology <SA2>
 F:404-476/Domain: serum albumin repeat homology #status atypical <SA3>
 F:23-75,74-83,96-112,111-122,145-190,189-198,220-266,265-273,286-300,299-311,335-376,37
 F:288/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 68.4%; Score 39; DB 1; Length 476;
 Best Local Similarity 63.6%; Pred. No. 12;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRQLTPYIQR 11
 |||:|:|:|
 DB 392 MKRQLTSFIEK 402

RESULT 15
 A01040
 molybdenum transport ATP-binding protein modC [imported] - Yersinia pestis (strain
 C:Species: Yersinia pestis
 C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 19-Jul-2002
 C:Accession: A01040
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.,
 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
 Nature 413, 523-527, 2001
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: A10140
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-359 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC89988.1; PID:GI5979210; GSPDB:GN00175
C:Genetics8
A:Gene: modC
C:Superfamily: molybdenum transport protein modC; ATP-binding cassette homology
Query Match 66.7%; Score 38; DB 2; Length 359;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Qy 2 KROUTPYIOR 11
Db 164 KREBLPYLER 173

Search completed: January 7, 2003, 17:15:08
Job time : 17 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 16:47:33 ; Search time 11 Seconds
(without alignments)
41.476 Million cell updates/sec

Title: US-09-623-006b-5
Sequence: 1 MKRQLTYRQR 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match Length	ID	Description
1	57	100.0	AP04_RAT	P02651 ratius norv
2	50	87.7	AP04_MOUSE	P06728 mus musculu
3	46	80.7	AP04_HUMAN	P06727 homo sapien
4	46	80.7	AP04_PAPAN	Q28758 papio anubi
5	46	80.7	AP04_MACPA	P33621 macaca fasc
6	41	71.9	MODC_ECOLI	P09833 escherichia
7	39	68.4	VTDB_RAT	P04376 rattus norv
8	38	66.7	TERO_BACFR	Q08425 bacteroides
9	38	66.7	TERO_BACFN	Q00937 bacteroides
10	38	66.7	TERO_PPERU	Q52360 prevotella
11	38	66.7	TERO_PPREIN	Q05197 prevotella
12	36	63.2	ML21_LACIC	P05179 lactococcus
13	36	63.2	AP04_PIG	Q46409 sus scrofa
14	36	63.2	VTDB_MOUSE	P21614 mus musculu
15	36	63.2	CHSG_ASPTU	P54267 aspergillus
16	36	63.2	CHSB_EMENT	Q00757 emericella
17	35	61.4	AGLK_RHIME	Q92379 rhizobium m
18	35	61.4	AHPF_XANCH	Q06465 xanthomonas
19	35	61.4	UBA1_MOUSE	Q02053 mus musculu
20	35	61.4	YB21_YEAST	P32386 saccharomyc
21	34	59.6	AP04_RAT	P04638 rattus norv
22	34	59.6	MTUD_BACSU	P42957 bacillus su
23	34	59.6	MTUD_BACSD	Q9681 bacillus ha
24	34	59.6	WKRI_MACED	Q9691 macropus eu
25	34	59.6	MCR_RAT	P22199 rattus norv
26	34	59.6	BGAL_BACME	Q52847 bacillus me
27	34	59.6	12294_HUMAN	Q94822 homo sapien
28	33	57.9	PMVK_DROME	Q94722 drosophila
29	33	57.9	AROB_LISIN	Q92881 listeria in
30	33	57.9	AROB_LISMO	Q94816 listeria mo
31	33	57.9	NOR_FUSOX	P23395 fusarium ox
32	33	57.9	NPRA_BACST	P43330 bacillus st
33	33	57.9	COA2_BPFJ3	P03624 bacterioph

34	33	57.9	652	1	MX1_RAT	P19588 rattus norv
35	32	56.1	100	1	AP02_HUMAN	P02652 homo sapien
36	32	56.1	105	1	AP01_PETMA	P07095 petromyzon
37	32	56.1	122	1	RLJ5_SCHPO	Q74904 schizosacch
38	32	56.1	157	1	NUSB_XYLPF	Q9583 xyella fas
39	32	56.1	158	1	NRDG_PASMU	Q95894 pasteurella
40	32	56.1	247	1	YORF_BACSU	P54474 bacillus su
41	32	56.1	300	1	RNH3_STRPY	Q99470 streptococc
42	32	56.1	310	1	YC30_GUTTH	Q78432 guillardi
43	32	56.1	310	1	YC62_MESVT	Q9mrt3 mesocistima
44	32	56.1	342	1	YB22_MYCTU	P71691 mycobacteri
45	32	56.1	359	1	Y564_MYCLE	Q9ccn9 mycobacteri

ALIGNMENTS

RESULT 1
AP04_RAT
ID AP04_RAT STANDARD; PRT; 391 AA.
AC P02651;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Apolipoprotein A-IV precursor (Apo-AIV).
GN APOA4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN 1;
RP SEQUENCE FROM N.A.
RX MEDLINE=86196059; PubMed=3009456;
RA Boguski M.S., Birkenmeier E.H., Elshourbagy N.A., Taylor J.M.,
RA Gordon J.I.;
RT "Evolution of the apolipoproteins. Structure of the rat apo-A-IV gene
RT and its relationship to the human genes for apo-A-I, C-III, and E";
RL J. Biol. Chem. 261:6398-6407(1986).
RN 2;
RP SEQUENCE FROM N.A.
RX MEDLINE=84298074; PubMed=6591177;
RA Boguski M.S., Elshourbagy N.A., Taylor J.M., Gordon J.I.;
RT "Rat apolipoprotein A-IV contains 13 tandem repetitions of a 22-amino
RT acid segment with amphipathic helical potential.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:5021-5025(1984).
RN 3;
RP SEQUENCE FROM N.A.
RX MEDLINE=87008540; PubMed=3020028;
RA Haddad I.A., Ordovas J.M., Fitzpatrick T., Karathanasis S.K.;
RT "Linkage, evolution, and expression of the rat apolipoprotein A-I, C-
RT III, and A-IV genes.";
RL J. Biol. Chem. 261:13268-13277(1986).
CC -I- FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND VLDL SECRETION AND
CC CATABOLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN
CC LIPISE BY APOC-II. POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJOR
CC COMPONENT OF HDL AND CHYLOMICRONS.
CC -I- SUBCELLULAR LOCATION: Extracellular.
CC -I- TISSUE SPECIFICITY: SECRETED IN PLASMA.
CC -I- DOMAIN: NINE OF THE THIRTEEN 22-AMINO ACID TANDEM REPEATS (EACH
CC 22-MER IS ACTUALLY A TANDEM ARRAY OF TWO, A AND B, RELATED 11-
CC MERS) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-
CC HELICAL, AND MANY OF THESE HELICES ARE AMPHIPATHIC. THEY MAY
CC THEREFORE SERVE AS LIPID-BINDING DOMAINS WITH LECITHIN:CHOLESTEROL
CC ACUTRANSFERASE (LCAT) ACTIVATING ABILITIES.
CC -I- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
CC -----
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CC -----
DR EMBL; M00002; AAA85909.1; -
DR EMBL; J02588; AAA40747.1; -
DR EMBL; M13508; AAA40748.1; -
DR PIR; A03095; LPRTA4.
DR PIR; A25214; A25214.
DR PIR; C24700; C24700.
DR InterPro; IPR000074; Apolipoprotein.
KW Pfam; PF01442; Apolipoprotein; 2.
KW Plasma; Lipid transport; HDL; Chylomicron; Repeat; Signal.
FT SIGNAL 1 20
FT CHAIN 21 391
FT DOMAIN 33 330
FT REPEAT 33 54
FT REPEAT 60 81
FT REPEAT 82 103
FT REPEAT 115 136
FT REPEAT 137 158
FT REPEAT 159 180
FT REPEAT 203 224
FT REPEAT 225 246
FT REPEAT 247 268
FT REPEAT 269 286
FT REPEAT 287 308
FT REPEAT 309 330
FT DOMAIN 374 385
FT VARIANT 253 253
SQ SEQUENCE 391 AA; 44456 MW; 24095004A809201D CRC64;

Query Match 100.0%; Score 57; DB 1; Length 391;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKROLTPYIOR 11
Db 153 MKROLTPYIOR 163

RESULT 2
AP04 MOUSE STANDARD; PRT; 395 AA.
AC P06728;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Apolipoprotein A-IV precursor (Apo-AIV).
GN APOA4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87089722; PubMed=3796595;
RA Williams S.C., Bruckheimer S.M., Lusis A.J., LeBoeuf R.C.,
RA Kinniburgh A.J.;
RT "Mouse apolipoprotein A-IV gene: nucleotide sequence and induction by
RT a high-lipid diet";
RL Mol. Cell. Biol. 6:3807-3814 (1986).
RN [2]
RP REVISIONS.
RA Kinniburgh A.J.;
RL Submitted (DEC-1986) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J, and 129/J.
RX MEDLINE=91286309; PubMed=1648102;
RA Rue K., Leete T.H.;
RT "Genetic variation in mouse apolipoprotein A-IV due to insertion and
RT deletion in a region of tandem repeats.";
RL J. Biol. Chem. 266:12715-12721 (1991).
CC -/- FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND VLDL SECRETION AND

```

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CC -----
CC CATABOLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN
CC LIPASE BY APOC-II; POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJOR
CC COMPONENT OF HDL AND CHYLOMICRONS.
CC -/- SUBCELLULAR LOCATION: Extracellular.
CC -/- TISSUE SPECIFICITY: SECRETED IN PLASMA.
CC -/- DOMAIN: NINE OF THE THIRTEEN 22-AMINO ACID TANDEM REPEATS (EACH
CC 22-MER IS ACTUALLY A TANDEM ARRAY OF TWO, A AND B, RELATED 11-
CC MERS) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-
CC HELICAL, AND MANY OF THESE HELICES ARE AMPHIPATHIC. THEY MAY
CC THEREFORE SERVE AS LIPID-BINDING DOMAINS WITH LECITHIN:CHOLESTEROL
CC ACYLTRANSFERASE (LCAT) ACTIVATING ABILITIES.
CC -/- POLYMORPHISM: THERE IS A POLYMORPHISM WITHIN A SERIES OF IMPERFECT
CC REPEATS ENCODING THE SEQUENCE E-Q-[AV]-Q. INSERTIONS OR DELETIONS
CC OF 12 NUCLEOTIDES HAVE GIVEN RISE TO THREE FORMS CHARACTERIZED BY
CC THREE (129), FOUR (C57BL/6), OR FIVE (M.CASTANEUS) COPIES OF THE
CC REPEAT UNIT.
CC -/- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; M13966; AAA37253.1; -
DR EMBL; M64249; AAA37215.1; -
DR EMBL; M64248; AAA37214.1; -
DR PIR; A25281; A25281.
DR MGD; MGI-88051; APOA4.
DR InterPro; IPR000074; Apolipoprotein.
DR Pfam; PF01442; Apolipoprotein; 2.
KW Plasma; Lipid transport; HDL; Chylomicron; Repeat; Signal;
KW Polymorphism.
FT SIGNAL 1 295
FT CHAIN 21 395
FT DOMAIN 33 330
FT REPEAT 33 54
FT REPEAT 60 81
FT REPEAT 82 103
FT REPEAT 115 136
FT REPEAT 137 158
FT REPEAT 159 180
FT REPEAT 181 202
FT REPEAT 203 224
FT REPEAT 225 246
FT REPEAT 247 268
FT REPEAT 269 286
FT REPEAT 287 308
FT REPEAT 309 330
FT DOMAIN 366 389
FT VARIANT 382 385
FT CONFLICT 15 15 MISSING (IN SOME STRAINS).
FT CONFLICT 63 63 Q -> K (IN REF. 1).
FT CONFLICT 207 207 E -> R (IN REF. 1).
FT CONFLICT 288 288 S -> A (IN REF. 1).
FT CONFLICT 294 295 RQ -> KA (IN REF. 1).
FT CONFLICT 315 316 NK -> GG (IN REF. 1).
SQ SEQUENCE 395 AA; 45029 MW; 5FE27D0236226257 CRC64;

Query Match 87.7%; Score 50; DB 1; Length 395;
Best Local Similarity 90.9%; Pred. No. 0.026;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKROLTPYIOR 11
Db 153 MKROLTPYIOR 163

RESULT 3
AP04 HUMAN
ID AP04_HUMAN STANDARD; PRT; 396 AA.

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AC P06727; (Rel. 06, Created)
 DT 01-FEB-1988 (Rel. 17, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Apolipoprotein A-IV precursor (Apo-AIV).
 GN APOA4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Intestine;
 RX MEDLINE=89194198; PubMed=2930771;
 RA Yang C., Gu Z.W., Xiong W., Rosseneu M., Yang H.X., Lee B.M.,
 RA Goto A.M., Jr., Chan L.;
 RT "The primary structure of human apolipoprotein A-IV.";
 RL Biochim. Biophys. Acta 1002:231-237(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87041474; PubMed=3095836;
 RA Karathanasis S.K., Oetgen P., Haddad I.A., Antonarakis S.E.;
 RT "Structure, evolution, and polymorphisms of the human apolipoprotein
 RT A4 gene (APOA4).";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:8457-8461(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86296629; PubMed=3755616;
 RA Karathanasis S.K., Yunis I.;
 RT "Structure, evolution, and tissue-specific synthesis of human
 RT apolipoprotein AIV.";
 RL Biochemistry 25:3962-3970(1986).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87250378; PubMed=3036793;
 RA Elmhoutbagy N.A., Walker D.W., Pak Y.K., Boguski M.S., Freeman M.,
 RA Gordon J.I., Taylor J.M.;
 RT "Structure and expression of the human apolipoprotein A-IV gene.";
 RL J. Biol. Chem. 262:7973-7981(1987).
 RN [5]
 RP SEQUENCE OF 21-396 FROM N.A.
 RX MEDLINE=8611885; PubMed=3080432;
 RA Elmhoutbagy N.A., Walker D.W., Boguski M.S., Gordon J.I., Taylor J.M.;
 RT "The nucleotide and derived amino acid sequence of human
 RT apolipoprotein A-IV mRNA and the close linkage of its gene to the
 RT genes of apolipoproteins A-I and C-III.";
 RL J. Biol. Chem. 261:1998-2002(1986).
 RN [6]
 RP SIGNAL SEQUENCE CLEAVAGE SITE.
 RX MEDLINE=84161950; PubMed=6706947;
 RA Gordon J.I., Bieganski C.L., Sims H.F., Sachdev O.P., Glickman R.M.,
 RA Struse A.W.;
 RT "Biosynthesis of human preapolipoprotein A-IV.";
 RL J. Biol. Chem. 259:468-474(1984).
 RN [7]
 RP REVIEW ON POLYMORPHISM.
 RA Lohse P., Brewer H.B. Jr.;
 RT "Genetic polymorphism of apolipoprotein A-IV.";
 RL Curr. Opin. Lipidol. 2:90-95(1991).
 RN [8]
 RP VARIANT A-IV*2.
 RX MEDLINE=90277616; PubMed=2351649;
 RA Lohse P., Kindt M.R., Rader D.J., Brewer H.B. Jr.;
 RT "Genetic polymorphism of human plasma apolipoprotein A-IV is due to
 RT nucleotide substitutions in the apolipoprotein A-IV gene.";
 RL J. Biol. Chem. 265:10061-10064(1990).
 RN [9]
 RP VARIANTS A-IV*0 AND A-IV*3.
 RX MEDLINE=90324273; PubMed=1973689;
 RA Lohse P., Kindt M.R., Rader D.J., Brewer H.B. Jr.;
 RT "Human plasma apolipoproteins A-IV*0 and A-IV*3. Molecular basis for
 RT two rare variants of apolipoprotein A-IV.";
 RL J. Biol. Chem. 265:12734-12739(1990).

RN [10]
 RP VARIANTS.
 RX MEDLINE=91310615; PubMed=1677358;
 RA Lohse P., Kindt M.R., Rader D.J., Brewer H.B. Jr.;
 RT "Three genetic variants of human plasma apolipoprotein A-IV: apoA-IV-
 RT 1(Tyr-347->Ser), apoA-IV-0(Lys-167->Glu, Gln-360->His), and apoA-IV-
 RT 3(Glu-165->Lys).";
 RL J. Biol. Chem. 266:13513-13518(1991).
 RN [11]
 RP ERRATUM.
 RA Lohse P., Kindt M.R., Rader D.J., Brewer H.B. Jr.;
 RL J. Biol. Chem. 266:19866-19866(1991).
 RN [12]
 RP VARIANT MET-13.
 RX MEDLINE=9223894; PubMed=1349197;
 RA von Eckardstein A., Funke H., Schulte M., Erten M., Schulte H.,
 RA Aasmann G.;
 RT "Nonyonymous polymorphic sites in the apolipoprotein (apo) A-IV
 RT gene are associated with changes in the concentration of apo B- and
 RT apo A-I-containing lipoproteins in a normal population.";
 RL Am. J. Hum. Genet. 50:1115-1126(1992).
 RN [13]
 RP VARIANT SER-147.
 RX MEDLINE=92144647; PubMed=1737067;
 RA Tananen H., Koskinen P., Merso J., Baumann M., Lukka M.,
 RA Kauppinen-Makelin R., Kontula K., Taskinen M.R., Manttari M.,
 RA Manninen V., Ehnholm C.;
 RT "A novel polymorphism of apolipoprotein A-IV is the result of an
 RT asparagine to serine substitution at residue 127.";
 RL Biochim. Biophys. Acta 1138:27-33(1992).
 RN [14]
 RP VARIANT A-IV*5.
 RX MEDLINE=93138374; PubMed=1487136;
 RA Kamboh M.I., Williams B.R., Law J.C., Aston C.E., Bunker C.H.,
 RA Ferrell R.E., Pollitzer W.S.;
 RT "Molecular basis of a unique African variant (A-IV 5) of human
 RT apolipoprotein A-IV and its significance in lipid metabolism.";
 RL Genet. Epidemiol. 9:379-388(1992).
 RN [15]
 RP VARIANT BUDAPEST-2 LYS-44; BUDAPEST-1 CYS-305 AND SER-367.
 RX MEDLINE=95245341; PubMed=7728150;
 RA Menzel H.J., Dieplinger H., Sanholzer C., Karadi I., Utermann G.,
 RA Csaszar A.;
 RT "Apolipoprotein A-IV polymorphism in the Hungarian population: gene
 RT frequencies, effect on lipid levels, and sequence of two new
 RT variants.";
 RL Hum. Mutat. 5:58-65(1995).
 RN [16]
 RP VARIANTS FCPL SEATTLE SER-161; LEU-178 AND GLN-264.
 RX MEDLINE=97114287; PubMed=8956036;
 RA Deeb S.S., Nevin D.N., Iwasaki L., Brunzell J.D.;
 RT "Two novel apolipoprotein A-IV variants in individuals with familial
 RT combined hyperlipidemia and diminished levels of lipoprotein lipase
 RT activity.";
 RL Hum. Mutat. 8:319-325(1996).
 CC -1- FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND VLDL SECRETION AND
 CC CATABOLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN
 CC LIPIASE BY APOC-II; POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJOR
 CC COMPONENT OF HDL AND CHYLOMICRONS.
 CC -1- TISSUE SPECIFICITY: SYNTHESIZED PRIMARILY IN THE INTESTINE.
 CC -1- SECRETED IN PLASMA.
 CC -1- DOMAIN: NINE OF THE THIRTEEN 22-AMINO ACID TANDEM REPEATS (EACH
 CC 22-MER IS ACTUALLY A TANDEM ARRAY OF TWO, A AND B, RELATED 11-
 CC MERS) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-
 CC HELICAL, AND MANY OF THESE HELICES ARE AMPHIPATHIC. THEY MAY
 CC THEREFORE SERVE AS LIPID-BINDING DOMAINS WITH LECTININ-CHOLESTEROL
 CC ACYLTRANSFERASE (LCAT) ACTIVATING ABILITIES.
 CC -1- POLYMORPHISM: EIGHT ALLELES HAVE BEEN CHARACTERIZED (APOA-IV*0
 CC TO APOA-IV*7). APOA-IV*1 IS THE MAJOR ALLELE (90%), IV*2 IS ALSO
 CC COMMON (8%), THE OTHERS ARE RARE ALLELES.
 CC -1- DISEASE: DEFECTS IN APOA4 MAY CONTRIBUTE, ALONG WITH DEFECTS IN
 CC OTHER GENES OR ENVIRONMENTAL FACTORS, TO THE DEVELOPMENT OF

CC FAMILIAL COMBINED HYPERLIPIDEMIA (FCHL).

CC -!- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.

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CC -----

DR EMBL; M14642; AAA51745.1; -

DR EMBL; M13629; CAA31955.1; -

DR EMBL; M14566; AAA51748.1; -

DR EMBL; J02758; AAA96731.1; -

DR EMBL; M13654; AAA51744.1; -

DR PIR; A26481; LPHU4.

DR PIR; A24449; A24448.

DR PIR; A29330; A29330.

DR PIR; A26280; A26280.

DR PIR; S02715; S02715.

DR HSSP; P02649; 1LE4.

DR SWISS-2DPAGE; P06727; HUMAN.

DR Genew; HGNC:602; APOA4.

DR MIM; 107690; -

DR InterPro; IPR000074; Apolipoprotein.

DR Pfam; PF01442; Apolipoprotein; 2.

KW Plasma; Lipid transport; HDL; Chylomicron; Repeat; Signal;

KW Disease mutation; Polymorphism.

FT SIGNAL 1 20

FT CHAIN 21 396 APOLIPOPROTEIN A-IV.

FT DOMAIN 33 330 13 X 22 AA APPROXIMATE TANDEM REPEATS.

FT REPEAT 33 54 1.

FT REPEAT 60 81 2.

FT REPEAT 82 103 3.

FT REPEAT 115 136 4.

FT REPEAT 137 158 5.

FT REPEAT 159 180 6.

FT REPEAT 181 202 7.

FT REPEAT 203 224 8.

FT REPEAT 225 246 9.

FT REPEAT 247 268 10.

FT REPEAT 269 286 11.

FT REPEAT 287 308 12.

FT REPEAT 309 330 13.

FT DOMAIN 372 389 GLU/GLN-RICH.

FT VARIANT 13 13 V -> M (IN APOA-IV*1D).

FT VARIANT 44 44 E -> K (IN BUDAPEST-2).

FT VARIANT 147 147 N -> S (IN APOA-IV*1B).

FT VARIANT 161 161 A -> S (IN SEATTLE-3; IN FCHL).

Query Match 80.7%; Score 46; DB 1; Length 396;

Best Local Similarity 72.7%; Pred. No. 0.16;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKRQLTPYIQR 11

Db 153 LRRQLTFYQQR 163

RESULT 4

ID APA4 PAPAN STANDARD; PRT; 401 AA.

AC Q28756;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE Apolipoprotein A-IV precursor (Apo-AIV) (fragment).

OS APOA4.

OS Papio anubis (olive baboon).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

OC Cercopithecinae; Papio.

OX NCBI_TaxID=9555;

RN [1]_TaxID=9555;

RP SEQUENCE FROM N.A.

RC TISSUE=Intestine;

RX MEDLINE=93340170; PubMed=8101842;

RA Hixson J.E., Kammerer C.M., Mott G.E., Birnbaum S.,

RA Powers P.K., Vandeberg J.L.;

RT "Baboon apolipoprotein A-IV. Identification of Lys-76-->Glu that

RT distinguishes two common isoforms and detection of length

RT polymorphisms at the carboxyl terminus.";

RL J. Biol. Chem. 268:15867-15873 (1993).

CC -!- FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND DETECTION OF LENGTH

CC CATABOLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN

CC LIPASE BY APOC-II; POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJOR

CC COMPONENT OF HDL AND CHYLOMICRONS.

CC -!- SUBCELLULAR LOCATION: Extracellular.

CC -!- TISSUE SPECIFICITY: SYNTHESIZED PRIMARILY IN THE INTESTINE.

CC SECRETED IN PLASMA.

CC -!- DOMAIN: NINE OF THE THIRTEEN 22-AMINO ACID TANDEM REPEATS (EACH

CC 22-MER IS ACTUALLY A TANDEM ARRAY OF TWO, A AND B, RELATED 11-

CC MERS) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-

CC HELICAL, AND MANY OF THESE HELICES ARE AMPHIPATHIC. THEY MAY

CC THEREFORE SERVE AS LIPID-BINDING DOMAINS WITH LECITHIN:CHOLESTEROL

CC ACYLTRANSFERASE (LCAT) ACTIVATING ABILITIES.

CC -!- POLYMORPHISM: THERE ARE TWO COMMON APOA-IV ISOFORMS, I (SHOWN

CC HERE) AND E. THE I ISOFORM IS ASSOCIATED WITH HIGHER LEVELS OF

CC HIGH DENSITY LIPOPROTEIN-C ON A HIGH CHOLESTEROL, SATURATED FAT

CC DIET.

CC -!- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.

CC -----

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CC -----

DR EMBL; L13174; AAA35379.1; -

DR HSSP; P02649; INFN.

DR InterPro; IPR000074; Apolipoprotein.

DR Pfam; PF01442; Apolipoprotein; 2.

KW Plasma; Lipid transport; HDL; Chylomicron; Repeat; Signal;

KW Polymorphism.

FT NON_TER 1 1

FT SIGNAL <1 4 POTENTIAL.

FT CHAIN 5 401 APOLIPOPROTEIN A-IV.

FT DOMAIN 17 314 13 X 22 AA APPROXIMATE TANDEM REPEATS.

FT REPEAT 17 38 1.

FT REPEAT 44 65 2.

FT REPEAT 66 87 3.

FT REPEAT 99 120 4.

FT REPEAT 121 142 5.

FT REPEAT 143 164 6.

FT REPEAT 165 186 7.

FT REPEAT 187 208 8.

FT REPEAT 209 230 9.

FT REPEAT 231 252 10.

FT REPEAT 253 270 11.

FT REPEAT 271 292 12.

FT REPEAT 293 314 13.

FT DOMAIN 356 394 GLU/GLN-RICH.

FT VARIANT 80 80 K -> E (IN ISOFORM E).

SQ SEQUENCE 401 AA; 46538 MW; 0A76D1284AA9837F CRC64;

Query Match 80.7%; Score 46; DB 1; Length 401;

Best Local Similarity 72.7%; Pred. No. 0.16;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKRQLTPYIQR 11

Db 137 LRRLTPYACR 147

RESULT 5
AF04_MACFA STANDARD; PRT; 429 AA.

AC P3621;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Apolipoprotein A-IV precursor (apo-AIV).
GN APOA4.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leukocyte;
RX MEDLINE=93192330; PubMed=9448212;
RA Osada J., Pocovi M., Nicolosi R.J., Schaefer E.J., Ordovas J.M.;
RT "Nucleotide sequences of the Macaca fascicularis apolipoprotein C-II
and A-IV genes."
RL Biochim. Biophys. Acta 1172:335-339(1993).
CC -1- FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND VLDL SECRETION AND
CATBOLOISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN
LIPASE BY APOC-II; POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJOR
COMPONENT OF HDL AND CHYLOMICRONS.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: SECRETED IN PLASMA.
CC -1- DOMAIN: NINE OF THE THIRTEEN 22-AMINO ACID TANDEM REPEATS (EACH
22-MER IS ACTUALLY A TANDEM ARRAY OF TWO, A AND B, RELATED 11-
MERS) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-
HELICAL, AND MANY OF THESE HELICES ARE AMPHIPATHIC. THEY MAY
THEREFORE SERVE AS LIPID-BINDING DOMAINS WITH LECTININ-CHOLESTEROL
ACYLTRANSFERASE (LCAT) ACTIVATING ABILITIES.
CC -1- SIMILARITY: BELONGS TO THE APOA1 / APOA4 / APOE FAMILY.
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CC -----
DR EMBL; X68361; CAA48421.1; -.
DR PIR; S29565; S29565.
DR PIR; S30195; S30195.
DR HSSP; P02649; INPN.
DR InterPro; IPR000074; Apolipoprotein.
DR Pfam; PF01442; Apolipoprotein_2.
KW Plasma; Lipid transport; HDL; Chylomicron; Repeat; Signal.
FT SIGNAL 1 20
FT CHAIN 21 429
FT DOMAIN 33 330 13 X 22 AA APPROXIMATE TANDEM REPEATS.
FT REPEAT 33 330 1.
FT REPEAT 60 81 2.
FT REPEAT 82 103 3.
FT REPEAT 115 136 4.
FT REPEAT 137 158 5.
FT REPEAT 159 180 6.
FT REPEAT 181 202 7.
FT REPEAT 203 224 8.
FT REPEAT 225 246 9.
FT REPEAT 247 268 10.
FT REPEAT 269 286 11.
FT REPEAT 287 308 12.
FT REPEAT 309 330 13.
FT DOMAIN 372 420 GLU/GLN-RICH.
SQ SEQUENCE 429 AA; 49876 MW; 3D458F551D0D60C CRC64;

Query Match 80.7%; Score 46; DB 1; Length 429;
Best Local Similarity 72.7%; Pred. No. 0.17;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRQLTPYACR 11
Db 153 LRRLTPYACR 163

RESULT 6

ID MODC_ECOLI STANDARD; PRT; 352 AA.

AC P09833;

DT 01-MAR-1989 (Rel. 10, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Molybdenum transport ATP-binding protein modC.

GN MODC OR CHLD OR NARD OR B0765.

OS Escherichia coli.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia.

OX NCBI_TaxID=562;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=K12;

RX MEDLINE=95394784; PubMed=7665460;

RA Maugin-Fulow J.A., Rosenthal J.K., Lee J.H., Deppenmeier U.,

RT Gunatalus R.P., Shanmugam K.T.;

RT "Genetic analysis of the modABCD (molybdate transport) operon of

Escherichia coli.";

RL J. Bacteriol. 177:4851-4856(1995).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=K12 / MG1000;

RX MEDLINE=96151473; PubMed=8564363;

RA Walenhorst H.M., Hemschemeyer S.K., Eichenlaub R.;

RT "Molecular analysis of the molybdate uptake operon, modABCD, of

Escherichia coli and modK, a regulatory gene.";

RL Microbiol. Res. 150:347-361(1995).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=K12;

RX MEDLINE=87194564; PubMed=3553151;

RA Johann S., Hinton S.W.;

RT "Cloning and nucleotide sequence of the chld locus.";

RL J. Bacteriol. 169:1911-1916(1987).

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN=K12 / MG1655;

RX MEDLINE=97426617; PubMed=9278503;

RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,

RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,

RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

RA Mau B., Shao Y.;

RT "The complete genome sequence of Escherichia coli K-12.";

RL Science 277:1453-1474(1997).

RN [5]

RP SEQUENCE FROM N.A.

RC STRAIN=K12;

RX MEDLINE=97061202; PubMed=8905232;

RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,

RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kaishimoto K.,

RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,

RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,

RA Sampei G., Seki Y., Tagami H., Takenoto K., Wada C., Yamamoto Y.,

RA Yano M., Horiuchi T.;

RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome

corresponding to the 12.7-28.0 min region on the linkage map.";

RT DNA Res. 3:137-155(1996).

CC -1- FUNCTION: PART OF THE BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM

FOR MOLYBDENUM. PROBABLY RESPONSIBLE FOR ENERGY COUPLING TO THE

TRANSPORT SYSTEM.

CC

CC -!- SUBCELLULAR LOCATION: Inner membrane-associated.
 CC -!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
 CC -----
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 CC -----
 CC EMBL; U27192; AAB60173.1; -;
 CC EMBL; M16182; AAB3840.1; -;
 CC EMBL; U07867; AAB06895.1; -;
 CC EMBL; L34009; AAB00837.1; -;
 CC EMBL; AE000179; AAC73852.1; -;
 CC EMBL; D90715; BAA35429.1; -;
 CC PIR; B26871; BVECHD.
 CC Ecogene; EG10152; modC.
 CC InterPro; IPR003593; AAA_ATPase.
 CC InterPro; IPR003439; ABC_transportr.
 CC InterPro; IPR004606; Mop.
 CC InterPro; IPR005116; TOBE.
 CC Pfam; PF00005; ABC_tran; 1.
 CC Pfam; PF03459; TOBE; 1.
 CC SMART; SM00382; AAA; 1.
 CC TIGRFAMs; TIGR00638; Mop; 1.
 CC PROSITE; PS00211; ABC_TRANSPORT; 1.
 KW Inner membrane; Transport; ATP-binding; Molybdenum; Complete proteome.
 FT NP_BIND 31 38 ATP (BY SIMILARITY).
 FT SALRDDR -> PHYAMTA (IN REF. 1, 4 AND 5).
 FT AALRIQADVSLVLPQPOOTSIRNVLRAKVNVDNQO
 FT CONFLICT 244 250
 FT VEVELEVGKTLWARSIPWARDLAKGLMLYAIKSVI
 FT TA -> LRYVPHSGRCFSFWYNSKPAFTIAGKSC
 FT (IN REF. 3).
 FT SQ SEQUENCE 352 AA; 39144 MW; 423E80EAZCIAFI44 CRC64;
 Query Match 71.9%; Score 41; DB 1; Length 352;
 Best Local Similarity 70.0%; Pred. No. 1.3;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 OY 2 KQSLTPYIQR 11
 Db 164 KRELLPYLQR 173
 RESULT 7
 ID VTDB RAT STANDARD; PRT; 476 AA.
 AC P04376;
 DT 20-WAR-1987 (Rel. 04, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Vitamin D-binding protein precursor (DBP) (Group-specific component)
 DE (GC-globulin) (VDB).
 DE GC OR DBP.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=91177870; PubMed=2007578;
 RA Ray K., Wang X., Zhao M., Cooke N.E.;
 RT "The rat vitamin D binding protein (Gc-globulin) gene. Structural
 RT analysis, functional and evolutionary correlations.";
 RL J. Biol. Chem. 266:6221-6229(1991).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=90094352; PubMed=2480956;
 RA McLeod J.F., Cooke N.E.;
 RT "The vitamin D-binding protein, alpha-fetoprotein, albumin multigene
 RT family: detection of transcripts in multiple tissues.";

RL J. Biol. Chem. 264:21760-21769(1989).
 RN [3]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=86140127; PubMed=2419332;
 RA Cooke N.E.;
 RT "Rat vitamin D binding protein. Determination of the full-length
 RT primary structure from cloned cDNA.";
 RL J. Biol. Chem. 261:3441-3450(1986).
 RN [4]
 RN SEQUENCE OF 17-40.
 RX MEDLINE=86229807; PubMed=3713442;
 RA Litwiler R.D., Fass D.N., Kumar R.;
 RT "The amino acid sequence of the NH2-terminal portion of rat and human
 RT vitamin D binding protein: evidence for a high degree of homology
 RT between rat and human vitamin D binding protein.";
 RL Life Sci. 38:2179-2184(1986).
 CC -!- FUNCTION: MULTIFUNCTIONAL PROTEIN FOUND IN PLASMA, ASCITIC FLUID,
 CC CEREBROSPINAL FLUID, AND URINE AND ON THE SURFACE OF MANY CELL
 CC TYPES. IN PLASMA, IT CARRIES THE VITAMIN D STEROLS AND PREVENTS
 CC POLYMERIZATION OF ACTIN BY BINDING ITS MONOMERS. DBP ASSOCIATES
 CC WITH MEMBRANE-BOUND IMMUNOGLOBULIN ON THE SURFACE OF B-LYMPHOCYTES
 CC AND WITH IGG FC RECEPTOR ON THE MEMBRANES OF T-LYMPHOCYTES.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE ALB/APP/VDB FAMILY.
 CC -!- SIMILARITY: CONTAINS 3 ALBUMIN DOMAINS.
 CC -----
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 CC -----
 CC EMBL; M60205; AAA41081.1; -;
 CC EMBL; M60197; AAA41081.1; JOINED.
 CC EMBL; M60198; AAA41081.1; JOINED.
 CC EMBL; M60199; AAA41081.1; JOINED.
 CC EMBL; M60200; AAA41081.1; JOINED.
 CC EMBL; M60201; AAA41081.1; JOINED.
 CC EMBL; M60202; AAA41081.1; JOINED.
 CC EMBL; M60203; AAA41081.1; JOINED.
 CC EMBL; M60204; AAA41081.1; JOINED.
 CC EMBL; M12450; AAA41080.1; -;
 CC EMBL; J05148; AAA41082.1; -;
 CC PIR; A38726; VYRTD.
 CC InterPro; IPR000264; Serum_albumin.
 CC Pfam; PF00273; transport_prot; 2.
 CC PRINTS; PR00802; SERUMALBUMIN.
 CC SMART; SM00103; ALBUMIN; 2.
 CC PROSITE; PS00212; ALBUMIN; 1.
 KW Albumin; Glycoprotein; Vitamin D; Transport; Plasma; Actin-binding;
 KW Repeat; Signal.
 FT SIGNAL 1
 FT CHAIN 1 16 VITAMIN D-BINDING PROTEIN.
 FT DOMAIN 17 476 ALBUMIN 1.
 FT DOMAIN 20 202 ALBUMIN 1.
 FT DOMAIN 208 388 ALBUMIN 2.
 FT DOMAIN 395 476 ALBUMIN 3.
 FT DISULFID 29 75 BY SIMILARITY.
 FT DISULFID 74 83 BY SIMILARITY.
 FT DISULFID 96 112 BY SIMILARITY.
 FT DISULFID 111 122 BY SIMILARITY.
 FT DISULFID 145 190 BY SIMILARITY.
 FT DISULFID 189 198 BY SIMILARITY.
 FT DISULFID 220 266 BY SIMILARITY.
 FT DISULFID 265 273 BY SIMILARITY.
 FT DISULFID 286 300 BY SIMILARITY.
 FT DISULFID 299 311 BY SIMILARITY.
 FT DISULFID 335 376 BY SIMILARITY.
 FT DISULFID 375 384 BY SIMILARITY.
 FT DISULFID 407 453 BY SIMILARITY.
 FT DISULFID 452 462 BY SIMILARITY.
 FT CARBOHYD 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT 288

FT CARBOHYD 432 432 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 132 132 E -> Q (IN REF. 2).
 FT CONFLICT 174 174 L -> P (IN REF. 3).
 FT CONFLICT 210 210 L -> S (IN REF. 2).
 SQ SEQUENCE 476 AA; 53544 MW; D3C7729BC44E221E CRC64;

Query Match 68.4%; Score 39; DB 1; Length 476;
 Best Local Similarity 63.6%; Pred. No. 4.5;
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKRQLTPYIOR 11
 Db 392 MKRQLTSFIEK 402

RESULT 8
 TETO_BACFR STANDARD; PRT; 641 AA.
 ID TETO_BACFR
 AC 008425;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tetracycline resistance protein tectQ (TetA(Q)2).
 GN TETO OR TET(Q).
 OS Bacteroides fragilis.
 OC Bacteroides; Bacteroidetes; Bacteroidales; Bacteroidaceae;
 OC Bacteroides.
 OX NCBI_TaxID=817;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1126;
 RX MEDLINE=94058212; PubMed=7916585.
 RA Lepine G., Lacroix J.-M., Walker C.B., Prognulske-Fox A.,
 RT "Sequencing of a tet(Q) gene isolated from Bacteroides fragilis
 1126.";
 RL Antimicrob. Agents Chemother. 37:2037-2041(1993).
 CC - FUNCTION: Abolishes the inhibitory effect of tetracyclin on
 protein synthesis by a non-covalent modification of the ribosomes.
 CC - SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
 CC - TETM/TETO SUBFAMILY.
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 CC -----
 DR EMBL: Z21523; CA979728.1; -;
 DR EMBL: Z21523; CA979727.1; ALT_INIT.
 DR HSSP: P13551; IDAR.
 DR InterPro: IPR000640; EFG_C.
 DR InterPro: IPR004161; EFTU_D2.
 DR InterPro: IPR000795; EF_GTPbind.
 DR InterPro: IPR005225; Small_GTP.
 DR Pfam: PF00009; GTP_EFTU; 1.
 DR Pfam: PF00679; EFG_C; 1.
 DR Pfam: PF03144; GTP_EFTU_D2; 1.
 DR PRINTS: PR00315; ELONGATNPFCT.
 DR TIGRFAMs: TIGR00231; small_GTP; 1.
 DR PROSITE: PS00301; EFACOR GTP; 1.
 KW Protein biosynthesis; Antibiotic resistance; GTP-binding.
 FT NP_BIND 10 17 GTP (BY SIMILARITY).
 FT NP_BIND 74 78 GTP (BY SIMILARITY).
 FT NP_BIND 128 131 GTP (BY SIMILARITY).
 SQ SEQUENCE 641 AA; 72523 MW; 4754576D8FD5347 CRC64;

Db 518 ROLTPYVFR 526

RESULT 9
 TETO_BACTN STANDARD; PRT; 641 AA.
 ID TETO_BACTN
 AC 000937;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tetracycline resistance protein tectQ (TetA(Q)1).
 GN TETO OR TET(Q).
 OS Bacteroides thetaiotaomicron.
 OC Bacteria; Bacteroidetes; Bacteroides; Bacteroidales; Bacteroidaceae;
 OC Bacteroides.
 OX NCBI_TaxID=818;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DOT;
 RX MEDLINE=92378171; PubMed=1339256;
 RA Nikolich M.P., Shoemaker N.B., Salyers A.A.;
 RT "A Bacteroides tetracycline resistance gene represents a new class of
 RT ribosome protection tetracycline resistance.";
 RL Antimicrob. Agents Chemother. 36:1005-1012(1992).
 RN [2]
 RP SEQUENCE OF 601-641 FROM N.A.
 RX MEDLINE=92234952; PubMed=1569023;
 RA Stevens A.W., Sanders J.M., Shoemaker N.B., Salyers A.A.;
 RT "Genes involved in production of plasmidlike forms by a Bacteroides
 RT conjugal regulatory element share amino acid homology with two-
 RT component regulatory systems.";
 RL J. Bacteriol. 174:2935-2942(1992).
 CC - FUNCTION: Abolishes the inhibitory effect of tetracyclin on
 protein synthesis by a non-covalent modification of the ribosomes.
 CC - SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
 CC - TETM/TETO SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: X58717; CA41552.1; -;
 DR EMBL: M81439; AAA22919.1; -;
 DR HSSP: P13551; IDAR.
 DR InterPro: IPR000640; EFG_C.
 DR InterPro: IPR004161; EFTU_D2.
 DR InterPro: IPR000795; EF_GTPbind.
 DR InterPro: IPR005225; Small_GTP.
 DR Pfam: PF00009; GTP_EFTU; 1.
 DR Pfam: PF00679; EFG_C; 1.
 DR Pfam: PF03144; GTP_EFTU_D2; 1.
 DR PRINTS: PR00315; ELONGATNPFCT.
 DR TIGRFAMs: TIGR00231; small_GTP; 1.
 DR PROSITE: PS00301; EFACOR GTP; 1.
 KW Protein biosynthesis; Antibiotic resistance; GTP-binding.
 FT NP_BIND 10 17 GTP (BY SIMILARITY).
 FT NP_BIND 74 78 GTP (BY SIMILARITY).
 FT NP_BIND 128 131 GTP (BY SIMILARITY).
 SQ SEQUENCE 641 AA; 72155 MW; 3402C31627315D5 CRC64;

Query Match 66.7%; Score 38; DB 1; Length 641;
 Best Local Similarity 77.8%; Pred. No. 9.6;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 ROLTPYIOR 11
 Db 518 ROLTPYVFR 526

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RESULT 10
TETQ_PRERU          STANDARD;          PRT;    641 AA.
ID  TETQ_PRERU
AC  Q52360;
DT  15-DEC-1998 (Rel. 37, Created)
DT  15-DEC-1998 (Rel. 37, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Tetracycline resistance protein tetQ (Tet(Q)).
GN  TETQ.
OS  Prevotella ruminicola (Bacteroides ruminicola).
OC  Bacteria; Bacteroidetes; Bacteroides; Bacteroidales; Prevotellaceae;
OC  Prevotella.
OX  NCBI_TaxID=839;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=223;
RX  MEDLINE=95031033; PubMed=7944364;
RA  Nikolich M.P., Hong G., Shoemaker N.B., Salyers A.A.;
RT  "Evidence for natural horizontal transfer of tetQ between bacteria
RT  that normally colonize humans and bacteria that normally colonize
RT  livestock.";
RL  Appl. Environ. Microbiol. 60:3255-3260(1994).
CC  -!- FUNCTION: Abolishes the inhibitory effect of tetracycline on
CC  protein synthesis by a non-covalent modification of the ribosomes.
CC  -!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC  TETM/TETO SUBFAMILY.
CC  -----
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CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
CC  EMBL; L33696; AAA62400.1; -.
CC  HSSP; P13551; 1DAR.
CC  InterPro; IPR000640; EFG_C.
CC  InterPro; IPR004161; EFTU_D2.
CC  InterPro; IPR000795; EF_GTPbind.
CC  InterPro; IPR005225; Small_GTP.
CC  Pfam; PF00009; GTP_EFTU; 1.
CC  Pfam; PF00679; EFG_C; 1.
CC  Pfam; PF03144; GTP_EFTU_D2; 1.
CC  PRINTS; PRO0315; ELONGATNFCT.
CC  TIGRFAMS; TIGR00231; small_GTP; 1.
CC  PROSITE; PS00301; EFACITOR_GTP; 1.
CC  Protein biosynthesis; Antibiotic resistance; GTP-binding.
CC  NP_BIND 10 17 GTP (BY SIMILARITY).
CC  NP_BIND 74 78 GTP (BY SIMILARITY).
CC  NP_BIND 128 131 GTP (BY SIMILARITY).
CC  SEQUENCE 641 AA; 72270 MW; 81233009D7593D38 CRC64;
CC  Query Match 66.7%; Score 38; DB 1; Length 641;
CC  Best Local Similarity 77.8%; Pred. No. 9.6;
CC  Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
CC  QY 3 ROLTPYIOR 11
CC  Db 518 RQLTPYVFR 526
CC  RESULT 11
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ID  TETQ_PREIN
AC  Q05157;
DT  15-DEC-1998 (Rel. 37, Created)
DT  15-DEC-1998 (Rel. 37, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Tetracycline resistance protein tetQ (Tet(Q)).
GN  TETQ OR TET(Q).
OS  Prevotella intermedia.
OC  Bacteria; Bacteroidetes; Bacteroides; Bacteroidales; Prevotellaceae;
OC  Prevotella.
OX  NCBI_TaxID=28131;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=PDRC-11;
RX  Bueno L.B., Presnail J.K., Walker C.B.;
RA  Submitted (OCT-1996) to the EMBL/GenBank/DBSJ databases.
CC  -!- FUNCTION: Abolishes the inhibitory effect of tetracycline on
CC  protein synthesis by a non-covalent modification of the ribosomes.
CC  -!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC  TETM/TETO SUBFAMILY.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
CC  EMBL; U73497; AAB51122.1; AUT_INIT.
CC  HSSP; P13551; 1DAR.
CC  InterPro; IPR000640; EFG_C.
CC  InterPro; IPR004161; EFTU_D2.
CC  InterPro; IPR000795; EF_GTPbind.
CC  InterPro; IPR005225; Small_GTP.
CC  Pfam; PF00009; GTP_EFTU; 1.
CC  Pfam; PF00679; EFG_C; 1.
CC  Pfam; PF03144; GTP_EFTU_D2; 1.
CC  PRINTS; PRO0315; ELONGATNFCT.
CC  TIGRFAMS; TIGR00231; small_GTP; 1.
CC  PROSITE; PS00301; EFACITOR_GTP; 1.
CC  Protein biosynthesis; Antibiotic resistance; GTP-binding.
CC  NP_BIND 10 17 GTP (BY SIMILARITY).
CC  NP_BIND 74 78 GTP (BY SIMILARITY).
CC  NP_BIND 128 131 GTP (BY SIMILARITY).
CC  SEQUENCE 654 AA; 74132 MW; 653CF3D193C3A1C CRC64;
CC  Query Match 66.7%; Score 38; DB 1; Length 654;
CC  Best Local Similarity 77.8%; Pred. No. 9.8;
CC  Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
CC  QY 3 ROLTPYIOR 11
CC  Db 518 RQLTPYVFR 526
CC  RESULT 12
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ID  ML21_LACLC          STANDARD;          PRT;    284 AA.
AC  P50179; Q93K25;
DT  01-OCT-1996 (Rel. 34, Created)
DT  15-JUN-2002 (Rel. 41, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  Modification methylase LlaDCHIA (EC 2.1.1.72) (Adenine-specific
DE  methyltransferase LlaDCHIA (M.LlaDCHIA) (M.LlaDCHIA) (M.LlaDCHIA) (M.LlaDCHIA OR LlaDCHIA OR LlaDCHIA).
GN  Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OS  Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OG  Plasmid pSRQ700.
OC  Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX  NCBI_TaxID=1359;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=DCH-4;
RX  MEDLINE=95314272; PubMed=7793939;
RA  Moineau S., Walker S.A., Vedamuthu E.R., Vandenberg P.A.;
RT  "Cloning and sequencing of LlaDCH1 restriction/modification genes
RT  from Lactococcus lactis and relatedness of this system to the
RT  Streptococcus pneumoniae DpnII system.";
RL  Appl. Environ. Microbiol. 61:2193-2202(1995).
RN  [2]
RP  ERRATUM.
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RA Moineau S., Walker S.A., Vedamuthu E.R., Vandenberg P.A.;
 RL Appl. Environ. Microbiol. 61:3514-3514(1995).
 RN [3]
 RP REVISIONS.
 RX MEDLINE=21360440; PubMed=11467810;
 RA Boucher I., Emond E., Parrot M., Moineau S.;
 RT "DNA sequence analysis of three *Lactococcus lactis* plasmids encoding
 RT phage resistance mechanisms";
 RL J. Dairy Sci. 84:1610-1620(2001).
 CC -1- FUNCTION: THIS METHYLASE RECOGNIZES THE DOUBLE-STRANDED SEQUENCE
 CC GATC, CAUSES SPECIFIC METHYLATION ON A-2 ON BOTH STRANDS, AND
 CC PROTECTS THE DNA FROM CLEAVAGE BY THE LADCHI ENDO nuclease.
 CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + DNA adenine = S-
 CC adenosyl-L-homocysteine + DNA 6-methylaminopurine.
 CC -1- MISCELLANEOUS: The LADCHI restriction system has two different
 CC methylases.
 CC -----
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 CC -----
 CC EMBL; U16027; AAK57808.1; -.
 CC HSSP; P04043; 2DPM.
 CC REBASE; 3662; M.LADCHIA.
 CC InterPro; IPR002294; D12N6_mtfase.
 CC InterPro; IPR002052; N6_Mtase.
 CC Pfam; PF02086; MethyltransferaseD12; 1.
 CC PRINTS; PR00505; D12N6MTFRASE.
 CC TIGRFAM; TIGR00571; dam; 1.
 CC PROSITE; PS00092; N6_MTASE; 1.
 CC TRANSFAS; Methyltransferase; Restriction system; Plasmid.
 CC SQUENCE 284 AA; 33078 MW; C46064217FC4B09 CRC64;
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 Query Match 63.2%; Score 36; DB 1; Length 284;
 Best Local Similarity 77.8%; Pred. No. 10;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 KRQLTPYIQ 10
 Db 21 KRQLTPHIQ 29
 RESULT 13
 AP04_PIG STANDARD; PRT; 382 AA.
 AC Q6409;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Apolipoprotein A-IV precursor (Apo-AIV).
 OS APOA4.
 GN Sus scrofa (pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Osada J., Iturzaide M., Calleja L., Gonzalez N., Pineiro A.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND VLDL SECRETION AND
 CC CATABOLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN
 CC LIPIASE BY APOC-II; POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJOR
 CC COMPONENT OF HDL AND CHYLOMICRONS.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: SECRETED IN PLASMA.
 CC -1- DOMAIN: NINE OF THE THIRTEEN 22-AMINO ACID TANDEM REPEATS (EACH
 CC 22-MER IS ACTUALLY A TANDEM ARRAY OF TWO, A AND B, RELATED 11-
 CC MERS) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-
 CC HELICAL, AND MANY OF THESE HELICES ARE AMPHIPATHIC. THEY MAY

CC THEREFORE SERVE AS LIPID-BINDING DOMAINS WITH LECTININ: CHOLESTEROL
 CC ACUTYANSEASE (LCAT) ACTIVATING ABILITIES.
 CC -1- SIMILARITY: BELONGS TO THE APOA / APOA4 / APOE FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AJ229666; CA11020.1; -.
 CC HSSP; P32851; 1BR0.
 CC InterPro; IPR000074; Apolipoprotein.
 CC Pfam; PF01442; Apolipoprotein; 2.
 CC KMW Plasma; Lipid transport; HDL; Chylomicron; Repeat; Signal.
 CC SIGNAL 1
 CC CHAIN 20
 CC FT 1 382
 CC FT DOMAIN 33 330
 CC FT REPEAT 33 54
 CC FT REPEAT 60 81
 CC FT REPEAT 82 103
 CC FT REPEAT 115 136
 CC FT REPEAT 137 158
 CC FT REPEAT 159 180
 CC FT REPEAT 181 202
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 CC FT REPEAT 287 308
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 CC FT DOMAIN 360 377
 CC SQUENCE 382 AA; 43294 MW; 2ACAB8A02D3379EF CRC64;
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 Best Local Similarity 54.5%; Pred. No. 14;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 KRQLTPYIOR 11
 Db 153 LQRQLKPYAER 163
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 VDB_MOUSE STANDARD; PRT; 472 AA.
 ID VDB_MOUSE
 AC P21614;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Vitamin D-binding protein precursor (DBP) (Group-specific component)
 DE (GC-globulin) (VDB) (Fragment).
 GN GC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=90353947; PubMed=1696927;
 RA Yang F., Bergeron J.W., Linehan L.A., Bailey P.A., Sakaguchi A.Y.,
 RA Bowman B.H.;
 RT "Mapping and conservation of the group-specific component gene in
 RT mouse";
 RL Genomics 7:509-516(1990).
 RN [2]
 RP SEQUENCE OF 13-34.
 RX MEDLINE=9211545; PubMed=3243374.
 RA Boke J.U., Litwiler R.D., Bell M.P., Fass D.N., McKean D.J.,
 RA Kumar R.;
 RT "The isolation, characterization and amino terminal sequence of the

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OM protein - protein search, using sw model

Run on: January 7, 2003, 17:15:04 (Search time 11 seconds
(without alignments)
18.952 Million cell updates/sec)

Title: US-09-623-006b-5
Perfect score: 57
Sequence: 1 MKROLTPYIOR 11

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Searched: 117078 seqs, 18951520 residues

Total number of hits satisfying chosen parameters: 117078

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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14: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB pep:*
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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	391	9 US-09-987-107-38	Sequence 38, Appl
2	50	87.7	391	10 US-09-800-729-208	Sequence 208, App
3	50	87.7	395	9 US-09-987-107-35	Sequence 35, Appl
4	46	80.7	396	9 US-09-987-107-33	Sequence 33, Appl
5	46	80.7	401	9 US-09-987-107-36	Sequence 36, Appl
6	46	80.7	429	9 US-09-987-107-34	Sequence 34, Appl
7	41	71.9	66	9 US-09-664-884-31	Sequence 31, Appl
8	36	63.2	382	9 US-09-987-107-37	Sequence 37, Appl
9	36	63.2	382	10 US-09-800-729-206	Sequence 206, App
10	36	63.2	640	10 US-09-815-242-11884	Sequence 11884, A
11	34	59.6	188	9 US-09-738-626-6600	Sequence 6600, Ap
12	34	59.6	368	10 US-09-815-242-5636	Sequence 5636, Ap
13	34	59.6	368	10 US-09-815-242-12393	Sequence 12393, A
14	33	57.9	178	10 US-09-216-393-137	Sequence 137, App
15	32	56.1	78	10 US-09-864-761-46908	Sequence 46908, A
16	32	56.1	378	9 US-09-971-536-46	Sequence 46, Appl
17	32	56.1	396	10 US-09-800-729-207	Sequence 207, App
18	31	54.4	89	10 US-09-864-761-36212	Sequence 36212, A
19	31	54.4	157	9 US-09-764-868-836	Sequence 836, App

20	31	54.4	268	10 US-09-925-637-60	Sequence 60, Appl
21	31	54.4	469	9 US-09-738-626-5350	Sequence 5350, Ap
22	31	54.4	639	10 US-09-925-301-1158	Sequence 1158, Ap
23	31	54.4	922	9 US-09-738-626-5476	Sequence 5476, Ap
24	30	52.6	42	10 US-09-864-761-46270	Sequence 46270, A
25	30	52.6	59	10 US-09-867-550-1796	Sequence 1796, Ap
26	30	52.6	130	9 US-09-854-133-33	Sequence 33, Appl
27	30	52.6	130	10 US-09-738-973-33	Sequence 33, Appl
28	30	52.6	169	10 US-09-867-550-642	Sequence 642, App
29	30	52.6	200	9 US-09-738-626-5477	Sequence 5477, Ap
30	30	52.6	215	10 US-09-925-297-660	Sequence 660, App
31	30	52.6	224	10 US-09-815-242-5715	Sequence 5715, Ap
32	30	52.6	230	10 US-09-815-242-12475	Sequence 12475, A
33	30	52.6	244	10 US-09-911-826A-9	Sequence 9, Appl
34	30	52.6	264	9 US-09-987-107-26	Sequence 26, Appl
35	30	52.6	264	9 US-09-987-107-27	Sequence 27, Appl
36	30	52.6	289	10 US-09-778-971-8	Sequence 8, Appl
37	30	52.6	316	10 US-09-815-242-13647	Sequence 13647, A
38	30	52.6	393	10 US-09-784-077-2	Sequence 2, Appl
39	30	52.6	430	10 US-09-799-777-62	Sequence 62, Appl
40	30	52.6	431	9 US-09-967-796-2	Sequence 2, Appl
41	30	52.6	499	10 US-09-778-971-7	Sequence 7, Appl
42	30	52.6	510	10 US-09-727-628-2	Sequence 11, Appl
43	30	52.6	510	10 US-09-821-232-11	Sequence 11, Appl
44	30	52.6	510	10 US-09-821-330-11	Sequence 11, Appl
45	30	52.6	510	10 US-09-921-329-11	Sequence 11, Appl

ALIGNMENTS

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RESULT 1
US-09-987-107-38
Sequence 38, Application US/09987107
Patent No. US20020156007A1
GENERAL INFORMATION:
APPLICANT: GRAVERSEN, Jonas
APPLICANT: MOESTRUP, Soren
TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
FILE REFERENCE: GRAVERSENIA
CURRENT APPLICATION NUMBER: US/09/987, 107
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/264, 022
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: DK PA2001 00057
PRIOR FILING DATE: 2001-01-15
PRIOR APPLICATION NUMBER: DK PA2000 01682
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PatentIn version 3.1
SEQ ID NO 38
LENGTH: 391
TYPE: PRT
ORGANISM: Rattus norvegicus
US-09-987-107-38
Query Match 100.0%; Score 57; DB 9; Length 391;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 11; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
QY 1 MKROLTPYIOR 11
DB 153 MKROLTPYIOR 163
RESULT 2
US-09-800-729-208
Sequence 208, Application US/09800729
Patent No. US20020068319A1
GENERAL INFORMATION:
APPLICANT: NI et al.
TITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: PZ044P1
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; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
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; ORGANISM: Homo sapiens
US-09-800-729-208
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Query Match      87.7%  Score 50; DB 10; Length 391;
Best Local Similarity 90.9%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 153 MKLQLTPYIQR 163
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RESULT 3

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US-09-987-107-35
; Sequence 35, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSEN1A
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-987-107-35
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Query Match      87.7%  Score 50; DB 9; Length 395;
Best Local Similarity 90.9%; Pred. No. 0.028;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Db 153 MKLQLTPYIQR 163
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RESULT 4

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; Sequence 33, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSEN1A
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
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; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-987-107-33
```

```
Query Match      80.7%  Score 46; DB 9; Length 396;
Best Local Similarity 72.7%; Pred. No. 0.17;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 MKRQLTPYIQR 11
   : |||||
Db 153 LRRQLTPYIQR 163
```

RESULT 5

```
US-09-987-107-36
; Sequence 36, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSEN1A
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Papio anubis
US-09-987-107-36
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Query Match      80.7%  Score 46; DB 9; Length 401;
Best Local Similarity 72.7%; Pred. No. 0.17;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 MKRQLTPYIQR 11
   : |||||
Db 137 LRRQLTPYIQR 147
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RESULT 6

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US-09-987-107-34
; Sequence 34, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSEN1A
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 429
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TYPE: PRT
ORGANISM: Macaca fascicularis
US-09-987-107-34

Query Match 80.7%; Score 46; DB 9; Length 429;
Best Local Similarity 72.7%; Pred. No. 0.18;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRQLTPYIOR 11
DB 153 LRRQLTPYIOR 163

RESULT 7
US-09-764-884-31
Sequence 31, Application US/09764884
Patent No. US20020161208A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT203
CURRENT APPLICATION NUMBER: US/09/764,884
PRIOR FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 31
LENGTH: 66
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (9)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-884-31

Query Match 71.9%; Score 41; DB 9; Length 66;
Best Local Similarity 70.0%; Pred. No. 0.22;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KROLTPYIOR 11
DB 27 KRELTPYIOR 36

RESULT 8
US-09-987-107-37
Sequence 37, Application US/09987107
Patent No. US20020156007A1
GENERAL INFORMATION:
APPLICANT: GRAVERSEN, Jonas
APPLICANT: MOESTRUP, Soren
TITLE OF INVENTION: APOLIPROTEINS ANALOGUES
FILE REFERENCE: GRAVERSENIA
CURRENT APPLICATION NUMBER: US/09/987,107
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/264,022
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: DK PA2001 00057
PRIOR FILING DATE: 2001-01-15
PRIOR APPLICATION NUMBER: DK PA2000 01682
PRIOR FILING DATE: 2000-11-10
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PatentIn version 3.1
SEQ ID NO 37
LENGTH: 382
TYPE: PRT
ORGANISM: Sus scrofa
US-09-987-107-37

Query Match 63.2%; Score 36; DB 9; Length 382;
Best Local Similarity 54.5%; Pred. No. 13;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKRQLTPYIOR 11
DB 153 LQRQLTPYIOR 163

RESULT 9
US-09-800-729-206
Sequence 206, Application US/09800729
Patent No. US20020068319A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: P2044P1
CURRENT APPLICATION NUMBER: US/09/800,729
PRIOR FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: PCT/US00/26013
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/155,709
PRIOR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 206
LENGTH: 382
TYPE: PRT
ORGANISM: Homo sapiens
US-09-800-729-206

Query Match 63.2%; Score 36; DB 10; Length 382;
Best Local Similarity 54.5%; Pred. No. 13;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKRQLTPYIOR 11
DB 153 LQRQLTPYIOR 163

RESULT 10
US-09-815-242-11884
Sequence 11884, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11884
LENGTH: 640

; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-815-242-11884

Query Match 63.2%; Score 36; DB 10; Length 640;
Best Local Similarity 70.0%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 KRQLTPYIQR 11
||| |||
Db 225 KXQLAAYIQR 234

RESULT 11
US-09-738-626-6600
; Sequence 6600, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAT, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: Patent in ver. 3.0
; SEQ ID NO 6600
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6600

Query Match 59.6%; Score 34; DB 9; Length 138;
Best Local Similarity 70.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKRQLTPYIQ 10
||| |||
Db 1 MKADLTYPYRQ 10

RESULT 12
US-09-815-242-5636
; Sequence 5636, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5636
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5636

Query Match 59.6%; Score 34; DB 10; Length 368;
Best Local Similarity 85.7%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 LTPYIQR 11
|||||
Db 193 LTPYIER 199

RESULT 13
US-09-815-242-12393
; Sequence 12393, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12393
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12393

Query Match 59.6%; Score 34; DB 10; Length 368;
Best Local Similarity 85.7%; Pred. No. 31;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 5 LTPYIOR 11
Db 193 LTPYIER 199

RESULT 14
US-09-216-393-137
; Sequence 137, Application US/09216393
; Patent No. US20010014447A1
; GENERAL INFORMATION:
; APPLICANT: Mlhausen, Michael James
; TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND
; FILE REFERENCE: TX-1-C2
; CURRENT APPLICATION NUMBER: US/09/216,393
; CURRENT FILING DATE: 1998-12-18
; EARLIER APPLICATION NUMBER: 08/994,825
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 137
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Toxoplasma gondii
US-09-216-393-137

Query Match 57.9%; Score 33; DB 10; Length 178;
Best Local Similarity 63.6%; Pred. No. 22;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKQQLTPYIOR 11
Db 166 LKQQLKRYRQ 176

RESULT 15
US-09-864-761-46908
; Sequence 46908, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aesomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 46908
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC009224.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.85
; OTHER INFORMATION: EST HUMAN HIT: BE895093.1, EVALUE 7.20e+00
; OTHER INFORMATION: SWISSPROT HIT: Q04719, EVALUE 3.10e+00
US-09-864-761-46908

Query Match 56.1%; Score 32; DB 10; Length 78;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 KQQLTPYIOR 11
Db 13 KTELTPGVQR 22

Search completed: January 7, 2003, 17:19:00
Job time : 24 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 7, 2003, 17:10:37 ; Search time 29 Seconds
(without alignments)
78.156 Million cell updates/sec

Title: US-09-623-006b-5
Perfect score: 57
Sequence: 1 MKRQLTPYICR 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_ivirus:*
16: sp_bacteriophage:*
17: sp_archaeophages:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	87.7	395	11 Q9DBN0	Q9dbn0 mus musculus
2	50	87.7	395	11 Q91XF8	Q91xf8 mus musculus
3	50	87.7	435	11 Q01488	Q01488 mus musculus
4	41	71.9	277	17 Q97AE7	Q97ae7 thermoplasma
5	41	71.9	308	16 Q8YVY5	Q8yvy5 anabaena sp
6	41	71.9	352	16 Q86OR6	Q86or6 salmonella
7	41	71.9	352	16 Q86R84	Q86r84 salmonella
8	41	71.9	352	16 Q8X4V7	Q8x4v7 escherichia
9	40	70.2	242	5 Q9XVQ2	Q9xvq2 caenorhabditis
10	38	66.7	359	16 Q8GXK6	Q8gxk6 caenorhabditis
11	38	66.7	657	2 P70882	P70882 bacteroides
12	37	64.9	224	16 Q8YBGO	Q8ybg0 bruceella me
13	37	64.9	342	16 Q9R9Q4	Q9r9q4 rhizobium me
14	37	64.9	342	16 Q8YBGO	Q8ybg0 bruceella me
15	37	64.9	342	16 Q8YBGO	Q8ybg0 bruceella me
16	37	64.9	342	16 Q8YBGO	Q8ybg0 bruceella me
17	37	64.9	342	16 Q8YBGO	Q8ybg0 bruceella me
18	37	64.9	342	16 Q8YBGO	Q8ybg0 bruceella me
19	37	64.9	342	16 Q8YBGO	Q8ybg0 bruceella me
20	37	64.9	342	16 Q8YBGO	Q8ybg0 bruceella me
21	37	64.9	342	16 Q8YBGO	Q8ybg0 bruceella me
22	37	64.9	342	16 Q8YBGO	Q8ybg0 bruceella me
23	37	64.9	342	16 Q8YBGO	Q8ybg0 bruceella me
24	37	64.9	342	16 Q8YBGO	Q8ybg0 bruceella me
25	37	64.9	342	16 Q8YBGO	Q8ybg0 bruceella me
26	37	64.9	342	16 Q8YBGO	Q8ybg0 bruceella me
27	37	64.9	342	16 Q8YBGO	Q8ybg0 bruceella me
28	37	64.9	342	16 Q8YBGO	Q8ybg0 bruceella me
29	37	64.9	342	16 Q8YBGO	Q8ybg0 bruceella me
30	37	64.9	342	16 Q8YBGO	Q8ybg0 bruceella me
31	37	64.9	342	16 Q8YBGO	Q8ybg0 bruceella me
32	37	64.9	342	16 Q8YBGO	Q8ybg0 bruceella me
33	37	64.9	342	16 Q8YBGO	Q8ybg0 bruceella me
34	37	64.9	342	16 Q8YBGO	Q8ybg0 bruceella me
35	37	64.9	342	16 Q8YBGO	Q8ybg0 bruceella me
36	37	64.9	342	16 Q8YBGO	Q8ybg0 bruceella me
37	37	64.9	342	16 Q8YBGO	Q8ybg0 bruceella me
38	37	64.9	342	16 Q8YBGO	Q8ybg0 bruceella me
39	37	64.9	342	16 Q8YBGO	Q8ybg0 bruceella me
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42	37	64.9	342	16 Q8YBGO	Q8ybg0 bruceella me
43	37	64.9	342	16 Q8YBGO	Q8ybg0 bruceella me
44	37	64.9	342	16 Q8YBGO	Q8ybg0 bruceella me
45	37	64.9	342	16 Q8YBGO	Q8ybg0 bruceella me

ALIGNMENTS

RESULT 1
ID Q9DBN0 PRELIMINARY: PRT, 395 AA.
AC Q9DBN0
DT 01-JUN-2001 (TrEMBLrel, 17, Created)
DT 01-JUN-2001 (TrEMBLrel, 17, Last sequence update)
DE Adult male liver cDNA, RIKEN full-length enriched library,
clone:1300002K10, full insert sequence.
GN APOA4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=LIVER;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai U., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi S., Yamanaka S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuohi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiraldi L.M., Staudt F., Suzuki K., Tomita M., Wagner L., Watanabe T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guetlinclish S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombert P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenwald C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyokawa K., Wang K.H., Welter C., Whitaker C., Wilting L.,
RA Wysshitzki A., Yoshida K., Hasegawa Y., Kawai H., Kontseki S.,
RA Hayashizaki Y.,
RA "Functional annotation of a full-length mouse cDNA collection.",
RL Nature 409:685-690 (2001).
DR EMBL; AK004856; BAB23620.1; -.

```

DR MGD; MGI:88051; APOA4.
DR InterPro: IPR000074; Apolipoprotein.
DR Pfam; PF01442; Apolipoprotein; 2.
SQ SEQUENCE 395 AA; 45044 MW; 4102084ACB0D182A CRC64;

Query Match 87.7%; Score 50; DB 11; Length 395;
Best Local Similarity 90.9%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKQLTPYIQR 11
DB 153 MKQLTPYIQR 163

RESULT 2
QY 153 MKQLTPYIQR 163
DB 153 MKQLTPYIQR 163

ID Q91XF8 PRELIMINARY; PRT; 395 AA.
AC Q91XF8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Unknown (protein for MGI:18592).
GN APOA4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010769; AAH10769.1; -.
DR MGD; MGI:88051; APOA4.
DR InterPro; IPR000074; Apolipoprotein.
DR Pfam; PF01442; Apolipoprotein; 2.
SQ SEQUENCE 395 AA; 45029 MW; C48B32ED441F71 CRC64;

Query Match 87.7%; Score 50; DB 11; Length 395;
Best Local Similarity 90.9%; Pred. No. 0.12;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKQLTPYIQR 11
DB 153 MKQLTPYIQR 163

RESULT 3
QY 153 MKQLTPYIQR 163
DB 153 MKQLTPYIQR 163

ID Q01488 PRELIMINARY; PRT; 435 AA.
AC Q01488;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Variant apolipoprotein A-IV precursor (APOA-IV).
GN APOA-4.
OS Mus musculus castaneus (southeastern Asian house mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10091;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=91286309; PubMed=1648102;
RA Ruee K., Leete T.H.;
RT "Genetic variation in mouse apolipoprotein A-IV due to insertion and deletion in a region of tandem repeats.";
RL J. Biol. Chem. 266:12715-12721 (1991).
CC -1- FUNCTION: MAY HAVE A ROLE IN CHYLOMICRONS AND VLDL SECRETION AND CATABOLISM. REQUIRED FOR EFFICIENT ACTIVATION OF LIPOPROTEIN LIPASE BY APOC-II; POTENT ACTIVATOR OF LCAT. APOA-IV IS A MAJOR COMPONENT OF HDL AND CHYLOMICRONS. IT MAY PLAY A ROLE IN THE INTRAVASCULAR METABOLISM OF HDL. POTENTIAL ROLE IN CELLULAR CHOLESTEROL EFFLUX.

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CC -1- TISSUE SPECIFICITY: INTESTINE, LIVER, AND PLASMA.
CC -1- MISCELLANEOUS: NINE OF THE THIRTEEN 22-AMINO ACID TANDEM REPEATS (EACH 22-MER IS ACTUALLY A TANDEM ARRAY OF TWO, A & B, RELATED 11-MERS) OCCURRING IN THIS SEQUENCE ARE PREDICTED TO BE HIGHLY ALPHA-HELICAL, & MANY OF THESE HELICES ARE ANPHIPATHIC. THEY MAY THEREFORE SERVE AS LIPID-BINDING DOMAINS WITH LECITHIN:CHOLESTEROL ACYLTRANSFERASE (LCAT) ACTIVATING ABILITIES.
CC -1- MISCELLANEOUS: THE APOA-IV POLYMORPHISMS ARE CLASSIFIED BASED ON THE OCCURRENCE OF THREE, FOUR, OR FIVE E-Q-A-Q/ E-Q-Q-Q/ E-Q-V-Q REPEAT UNITS.
DR EMBL; M64250; AAA37216.1; -.
DR InterPro; IPR000074; Apolipoprotein.
DR Pfam; PF01442; Apolipoprotein; 2.
KW Lipid transport; HDL; VLDL; Chylomicron; Repeat; Signal; Liver;
KW Plasma; Multigene family; Polymorphism; Cholesterol metabolism.
FT SIGNAL 1 20
FT CHAIN 21 435 VARIANT APOLIPOPROTEIN A-IV.
FT DOMAIN 374 393 TANDEM REPEATS.
FT REPEAT 374 377 1.
FT REPEAT 378 381 2.
FT REPEAT 382 385 3.
FT REPEAT 386 389 4.
FT REPEAT 390 393 5.
SQ SEQUENCE 435 AA; 49254 MW; B2AF55EEA8E456B2 CRC64;

Query Match 87.7%; Score 50; DB 11; Length 435;
Best Local Similarity 90.9%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKQLTPYIQR 11
DB 153 MKQLTPYIQR 163

RESULT 4
QY 153 MKQLTPYIQR 163
DB 153 MKQLTPYIQR 163

ID Q97AE7 PRELIMINARY; PRT; 277 AA.
AC Q97AE7;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE DNA adenine modification methylase.
GN TV0863 OR TVG0884813.
OS Thermoplasma volcanium.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Thermoplasmataceae; Thermoplasma.
OX NCBI_TaxID=50339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GSS1 / DSM 4299 / JCM 9571;
RX MEDLINE=20570466; PubMed=1121031;
RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
RA Kawashima-Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
RA Nunohiba T., Yamamoto Y., Atamaki H., Makino K., Suzuki M.;
RT "Archaeal adaptation to higher temperatures revealed by genomic sequence of Thermoplasma volcanium";
RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262 (2000).
DR EMBL; AP000994; BAB60005.1; -.
DR InterPro; IPR002294; D12N6_mtfase.
DR InterPro; IPR002052; N6_Mtase.
DR Pfam; PF02086; Methyltransferase; 1.
DR PRINTS; PR00505; D12N6MTFRASE.
DR TIGRPFAM; TIGR00571; dam; 1.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN 1.
KW Methyltransferase; Complete proteome.
SQ SEQUENCE 277 AA; 32045 MW; D894579F7476CEB3 CRC64;

Query Match 71.9%; Score 41; DB 17; Length 277;
Best Local Similarity 80.0%; Pred. No. 4.9;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KRLTPYIQR 11
DB 2 KRLTPYIQR 11

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Db 18 KROLIPYMR 27

RESULT 5

08YV5

AC 08YV5; PRELIMINARY; PRT; 308 AA.

DT 01-MAR-2002 (TReMBLrel. 20, Created)

DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)

DE Permease protein of sugar ABC transporter.

OS ALR0738.

OC Anabaena sp. (strain PCC 7120).

OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.

OX NCBI_TaxID=103690;

RN (1)

RP SEQUENCE FROM N.A.

RX MEDLINE=21595285; PubMed=11759840;

RA Kaneko T., Nakamura Y., Molk C.P., Kuritz T., Sasamoto S.,

RA Watanabe A., Iriyuchi M., Ishikawa A., Kawashina K., Kimura T.,

RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,

RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,

RA Yasuda M., Tabata S.,

RT "Complete genomic sequence of the filamentous nitrogen-fixing

cyanobacterium Anabaena sp. strain PCC 7120."

RL DNA Res. 8:205-213(2001).

EMBL; AB003583; BAB72695.1; -.

DR InterPro; IPR000515; BPD transp.

DR Pfam; PF00528; BPD_transp; 1.

KM Complete proteome.

SQ SEQUENCE 308 AA; 34267 MW; A7B386115F8642C0 CRC64;

Query Match

Best Local Similarity 71.9%; Score 41; DB 16; Length 308;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKROLTPYI 9

Db 12 IKROLTPYL 20

RESULT 6

08ZOR6

ID 08ZOR6; PRELIMINARY; PRT; 352 AA.

DT 01-MAR-2002 (TReMBLrel. 20, Created)

DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)

DE ABC superfamily (atp_bind), molybdate transporter.

GN WDC OR STW0783.

OS Salmonella typhimurium.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Salmonella.

OX NCBI_TaxID=602;

RN (1)

RP SEQUENCE FROM N.A.

RC STRAIN=IT2 / SGC1412 / ATCC 700720;

RX MEDLINE=21534948; PubMed=11677609;

RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,

RA Courtney L., Portolillo S., Ali J., Dante M., Du S., Layman D.,

RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,

RA Ryan E., Sun H., Flores L., Miller W., Stoneking T., Nhan M.,

RA Waterston R., Wilson R.K.;

RT "Complete genome sequence of Salmonella enterica serovar Typhimurium

LT2."

EMBL; AB008732; AAL19721.1; -.

DR InterPro; IPR003593; AAA_Atpase.

DR InterPro; IPR004339; ABC_transporter.

DR InterPro; IPR004606; MOP.

DR Pfam; PF00005; ABC_tran; 1.

DR Pfam; PF03459; TOBE; 1.

DR SMART; SM00382; AAA; 1.

DR TIGRfam; TIGR00638; MOP; 1.

DR PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.

KM Complete proteome.

SQ SEQUENCE 352 AA; 39055 MW; 65137E645711AAB5 CRC64;

Query Match

Best Local Similarity 71.9%; Score 41; DB 16; Length 352;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KROLTPYQR 11

Db 164 KRELTPYQR 173

RESULT 7

08ZBA4

ID 08ZBA4; PRELIMINARY; PRT; 352 AA.

DT 01-MAR-2002 (TReMBLrel. 20, Created)

DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)

DE Molybdenum transport ATP-binding protein ModC.

GN STY0816.

OS Salmonella typhi.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Salmonella.

OX NCBI_TaxID=601;

RN (1)

RP SEQUENCE FROM N.A.

RC STRAIN=CT18;

RX MEDLINE=21534947; PubMed=11677608;

RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,

RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,

RA Baker S., Basham P., Brooks K., Chillingworth T., Connor P.,

RA Cronin A., Davis P., Davies K.M., Dowd L., White N., Farrar J.,

RA Felwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jagels K.,

RA Krogh A., Larsen T.S., Leather S., Moulé S., O'Garra P., Parry C.,

RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,

RA Whitehead S., Barrett B.G.;

RT "Complete genome sequence of a multiple drug resistant Salmonella

enterica serovar Typhi CT18."

RL Nature 413:848-852(2001).

EMBL; AL627268; CAD05231.1; -.

DR InterPro; IPR003593; AAA_Atpase.

DR InterPro; IPR004339; ABC_transporter.

DR InterPro; IPR005116; TOBE.

DR Pfam; PF00005; ABC_tran; 1.

DR Pfam; PF03459; TOBE; 1.

DR SMART; SM00382; AAA; 1.

DR TIGRfam; TIGR00638; MOP; 1.

DR PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.

KM ATP-binding; Complete proteome.

SQ SEQUENCE 352 AA; 39111 MW; 30E56C25FD1D6683 CRC64;

Query Match

Best Local Similarity 70.0%; Score 41; DB 16; Length 352;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KROLTPYQR 11

Db 164 KRELTPYQR 173

RESULT 8

08X4V7

ID 08X4V7; PRELIMINARY; PRT; 352 AA.

DT 01-MAR-2002 (TReMBLrel. 20, Created)

DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)

DE ATP-binding component of molybdate transport (ATP-binding component of

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DE molybdate transport system).
GN MODC OR Z0935 OR ECS0793.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=83334;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
DR EMBL; AE005254; AAC55094.1; -.
DR EMBL; AF002553; BAB34216.1; -.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transportr.
DR InterPro; IPR004606; Mop-.
DR InterPro; IPR005116; TOBE
DR Pfam; PF00005; ABC_tran; 1.
DR Pfam; PF03459; TOBE; 1.
DR SMART; SM00382; AAA; 1.
DR TIGRFAMs; TIGR00638; Mop; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 352 AA; 39086 MW; 15D9CE74511AFD88 CRC64;

Query Match 71.9%; Score 41; DB 16; Length 352;
Best Local Similarity 70.0%; Pred. No. 6.2;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 KRQLTPYIQR 11
Db 164 KRELLPYLQR 173

RESULT 9
Q9XVQ2 PRELIMINARY; PRT; 242 AA.
AC Q9XVQ2;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE F15D3.7 protein.
GN F15D3.7
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]_
RP SEQUENCE FROM N.A.
RA White S.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]_
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;

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RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z81063; CAB02956.1; -.
SQ SEQUENCE 242 AA; 25066 MW; 064B8C2B5D8C3729 CRC64;

Query Match 70.2%; Score 40; DB 5; Length 242;
Best Local Similarity 60.0%; Pred. No. 6.7;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRQLTPYIQ 10
Db 71 VSRQWTPYVQ 80

RESULT 10
Q8ZGX6 PRELIMINARY; PRT; 359 AA.
ID Q8ZGX6;
AC Q8ZGX6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Molybdenum transport ATP-binding protein ModC.
GN MODC OR YP01147.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Yersinia.
OX NCBI_TaxID=632;
RN [1]_
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / BIOVAR ORIENTALIS;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
DR EMBL; AJ414146; CAC89988.1; -.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transportr.
DR InterPro; IPR004606; Mop.
DR InterPro; IPR005116; TOBE.
DR Pfam; PF00005; ABC_tran; 1.
DR Pfam; PF03459; TOBE; 1.
DR ProDom; PD000006; ABC_transportr; 1.
DR SMART; SM00382; AAA; 1.
DR TIGRFAMs; TIGR00638; Mop; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
KW ATP-binding; Complete proteome.
SQ SEQUENCE 359 AA; 39693 MW; B913D24A67DBD861 CRC64;

Query Match 66.7%; Score 38; DB 16; Length 359;
Best Local Similarity 60.0%; Pred. No. 25;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 KRQLTPYIQR 11
Db 164 KRELLPYLQR 173

RESULT 11
P70882 PRELIMINARY; PRT; 657 AA.
AC P70882;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE TETA(Q)3 protein.
GN TETA.

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RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Sebubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura Y.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.F., Eisen J.A., Karp P.D., Bovee D. Sr., Woo L.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RA "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58.";
RL Science 294:2317-2323(2001).
RN [2]
RX SEQUENCE FROM N.A.
RP MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houniel K., Gordon J., Vaudin M., Iatchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gursun J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RA "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58.";
RL Science 294:2323-2328(2001).
DR EMBL; AE009264; AAL44154.1; -.
DR EMBL; AE008348; AAK90049.1; -.
KW Complete proteome.
SQ SEQUENCE 342 AA; 37557 MW; D657A36A326D9C91 CRC64;

Query Match 64.9%; Score 37; DB 16; Length 342;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 QUTPYTOR 11
Db 122 QUTPYTOR 129

RESULT 15
Q9Z8Q3
ID Q9Z8Q3 PRELIMINARY; PRT; 515 AA.
AC Q9Z8Q3;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein CPN0285.
GN CPN0285 OR CPJ0285 OR CP0473.
OS Chlamydia pneumoniae (Chlamydiales; Chlamydiales; Chlamydiales).
OC Bacteria; Chlamydiales; Chlamydiales; Chlamydiales.
OX NCBI_TaxID=83558;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=CWL029;
RC MEDLINE=99206606; PubMed=10123388;
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN=ARJ9;
RC MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Baas S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae ARJ9.";
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
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RP SEQUENCE FROM N.A.
RC STRAIN=J138;
RX MEDLINE=20330349; PubMed=10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CWL029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).
DR EMBL; AE001613; AAD18434.1; -.
DR EMBL; AE002208; AAF38307.1; -.
DR EMBL; AP002546; BAA98495.1; -.
DR TIGR; CP0473; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 515 AA; 58173 MW; ED7525166A1A70AD CRC64;

Query Match 64.9%; Score 37; DB 16; Length 515;
Best Local Similarity 60.0%; Pred. No. 57;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KRQLTPYTOR 11
Db 271 KRKLTPHMQK 280

Search completed: January 7, 2003, 17:14:46
Job time : 32 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 7, 2003, 17:14:14 ; Search time 24 seconds
(without alignments)
32.485 Million cell updates/sec

Title: US-09-623-006B-5
Perfect score: 57
Sequence: 1 MKROLTPYIOR 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262191 seqs, 70875818 residues

Total number of hits satisfying chosen parameters: 262191

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:
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2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	71.9	352	6	US-10-287-274-448
2	37	64.9	343	1	PCT-US02-24310-101
3	35	61.4	62	1	PCT-US02-32727-21317
4	35	61.4	62	6	US-10-057-498-21317
5	34	59.6	278	5	US-09-724-676-55111
6	34	59.6	278	5	US-09-724-676-55111
7	34	59.6	278	5	US-09-724-676-55111
8	34	59.6	278	5	US-09-724-676-55111
9	33	57.9	244	5	US-09-724-676-55112
10	33	57.9	244	5	US-09-724-676-55112
11	32	56.1	263	5	US-09-134-000C-4795
12	32	56.1	373	5	US-09-134-000C-4795
13	32	56.1	391	6	US-10-092-411A-3952
14	32	56.1	506	5	US-09-724-676-71633
15	32	56.1	506	5	US-09-724-676-71633
16	32	56.1	537	5	US-09-724-676-71621
17	32	56.1	537	5	US-09-724-676-71621
18	32	56.1	545	5	US-09-724-676-71632
19	32	56.1	545	5	US-09-724-676-71632
20	32	56.1	545	5	US-09-724-676-71632
21	32	56.1	555	5	US-09-724-676-71631
22	32	56.1	755	5	US-09-724-676-71628
23	32	56.1	755	5	US-09-724-676-71628
24	32	56.1	785	5	US-09-724-676-71630
25	32	56.1	785	5	US-09-724-676-71630
26	32	56.1	1138	5	US-09-724-676-71629

27	32	56.1	2404	6	US-10-092-411A-3464	Sequence 3464, Ap
28	32	56.1	4649	1	PCT-US02-32851-10	Sequence 10, Appl
29	31	54.4	83	6	US-10-203-138A-13274	Sequence 13274, A
30	31	54.4	263	6	US-10-092-411A-4941	Sequence 4941, Ap
31	31	54.4	279	5	US-09-134-000C-5300	Sequence 5300, Ap
32	31	54.4	295	6	US-10-288-930-1155	Sequence 1155, Ap
33	31	54.4	311	5	US-09-724-676-52655	Sequence 52655, A
34	31	54.4	311	5	US-09-724-676-52655	Sequence 52655, A
35	31	54.4	366	6	US-10-092-411A-5067	Sequence 5067, Ap
36	31	54.4	418	5	US-09-724-676-73361	Sequence 73361, A
37	31	54.4	418	5	US-09-724-676-73361	Sequence 73361, A
38	31	54.4	418	5	US-09-724-676-73361	Sequence 73361, A
39	31	54.4	418	5	US-09-724-676-73361	Sequence 73361, A
40	31	54.4	509	1	PCT-US02-37760-101	Sequence 101, App
41	31	54.4	509	6	US-10-214-812-2	Sequence 2, Appl1
42	31	54.4	509	6	US-10-214-812-3	Sequence 3, Appl1
43	31	54.4	509	6	US-10-215-224-2	Sequence 2, Appl1
44	31	54.4	509	6	US-10-215-224-3	Sequence 3, Appl1
45	31	54.4	627	5	US-09-724-676-73362	Sequence 73362, A

ALIGNMENTS

```

RESULT 1
US-10-287-274-448
; Sequence 448, Application US/10287274
; GENERAL INFORMATION:
; APPLICANT: Foresyth, R. Allyn
; APPLICANT: Zykkind, Judith
; TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERETO
; FILE REFERENCE: ELITRA, 008DV1
; CURRENT APPLICATION NUMBER: US/10/287,274
; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 60/164415
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: US 09/711164
; PRIOR FILING DATE: 2000-11-09
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 448
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-287-274-448

Query Match      71.9%; Score 41; DB 6; Length 352;
Best Local Similarity 70.0%; Pred. No. 1.8;
Matches      7; Conservative      2; Mismatches      1; Indels      0; Gaps      0;

QY      2      MKROLTPYIOR 11
DB      164      KRELTPYIOR 173

RESULT 2
PCT-US02-24310-101
; Sequence 101, Application PC/RUS0224310
; GENERAL INFORMATION:
; APPLICANT: CUBIST PHARMACEUTICALS, INC.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATING TO THE DAPTOMYCIN
; FILE REFERENCE: CUB-12 PCT CIP
; CURRENT APPLICATION NUMBER: PCT/US02/44310
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: PCT/US01/32354
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 60/310,385
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 60/379,866
; PRIOR FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 170

```

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 101
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Streptomyces roseosporus
PCT-US02-24310-101

Query Match 64.9%; Score 37; DB 1; Length 343;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKRQLTPYIQ 10
|:|:|:|:|:
Db 151 MQRELTPYAE 160

RESULT 3
PCT-US02-32727-21317
; Sequence 21317, Application PC/TUS0232727
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; APPLICANT: Bhatia, Ajay
; APPLICANT: Maisonneuve, Jean Francois
; APPLICANT: Zhang, Yanni
; APPLICANT: Wang, Siging
; APPLICANT: Jen, Shyian
; APPLICANT: Lodes, Michael
; APPLICANT: Benson, Darin
; APPLICANT: Jones, Robert
; APPLICANT: Carter, Barrick
; APPLICANT: Barth, Brenda
; APPLICANT: Douglass, John
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121-514C1
; CURRENT APPLICATION NUMBER: PCT/US02/32727
; CURRENT FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 30992
; SEQ ID NO 21317
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Propioni acnes
PCT-US02-32727-21317

Query Match 61.4%; Score 35; DB 1; Length 62;
Best Local Similarity 85.7%; Pred. No. 5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 QLTPYIQ 10
|:|:|:|:|:
Db 12 QLTPYLQ 18

RESULT 4
US-10-057-498-21317
; Sequence 21317, Application US/10057498
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Skeiky, Yasir
; APPLICANT: Persing, David
; TITLE OF INVENTION: Compositions and Methods for the Therapy and Diagnosis of Acnes
; FILE REFERENCE: 210121-514
; CURRENT APPLICATION NUMBER: US/10/057,498
; CURRENT FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 29212
; SEQ ID NO 21317
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Propioni acnes
US-10-057-498-21317

Query Match 61.4%; Score 35; DB 6; Length 62;

Best Local Similarity 85.7%; Pred. No. 5;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 QLTPYIQ 10
|:|:|:|:|:
Db 12 QLTPYLQ 18

RESULT 5
US-09-724-676-55111
; Sequence 55111, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55111
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-55111

Query Match 59.6%; Score 34; DB 5; Length 278;
Best Local Similarity 55.6%; Pred. No. 35;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RQLTPYIQ 11
|:|:|:|:|:
Db 183 REVTPYIKK 191

RESULT 6
US-09-724-676A-55111
; Sequence 55111, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55111
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-55111

Query Match 59.6%; Score 34; DB 5; Length 278;
Best Local Similarity 55.6%; Pred. No. 35;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RQLTPYIQ 11
|:|:|:|:|:
Db 183 REVTPYIKK 191

RESULT 7
US-09-724-676-55112
; Sequence 55112, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55112
; LENGTH: 486

```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-55112

```

```

Query Match
Best Local Similarity 59.6%; Score 34; DB 5; Length 486;
Pred. No. 62;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 QUTPYIQR 11
|::|::|::|
Db 183 REVTPYIKK 191

```

```

RESULT 8
US-09-724-676A-55112
; Sequence 55112, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variance of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55112
; LENGTH: 486
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-55112

```

```

Query Match
Best Local Similarity 59.6%; Score 34; DB 5; Length 486;
Pred. No. 62;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 QUTPYIQR 11
|::|::|::|
Db 183 REVTPYIKK 191

```

```

RESULT 9
US-09-134-000C-4795
; Sequence 4795, Application US/09134000C
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4795
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4795

```

```

Query Match
Best Local Similarity 57.9%; Score 33; DB 5; Length 244;
Pred. No. 49;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 3 QUTPYIQR 11
|::|::|::|
Db 22 RQAPYIQR 30

```

```

RESULT 10
US-09-134-000C-6023
; Sequence 6023, Application US/09134000C
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al

```

```

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6023
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6023

```

```

Query Match
Best Local Similarity 56.1%; Score 32; DB 5; Length 263;
Pred. No. 84;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 3 QUTPYIQR 11
|::|::|::|
Db 120 KQTPYFRK 128

```

```

RESULT 11
US-09-134-000C-4179
; Sequence 4179, Application US/09134000C
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4179
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4179

```

```

Query Match
Best Local Similarity 56.1%; Score 32; DB 5; Length 373;
Pred. No. 1,2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 4 QUTPYIQR 10
|::|::|::|
Db 310 QUTPYIQR 316

```

```

RESULT 12
US-10-092-411A-3952
; Sequence 3952, Application US/10092411A
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: 032796-101
; CURRENT APPLICATION NUMBER: US/10/092,411A
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 09/134,001
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5676
; SEQ ID NO 3952
; LENGTH: 391
; TYPE: PRT

```

; ORGANISM: Staphylococcus epidermidis
US-10-092-411A-3952

Query Match 56.1%; Score 32; DB 6; Length 391;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 KRQLTPYIQR 11
| :||| |
Db 141 KMWTPYSOR 150

RESULT 13

US-09-724-676-71633
; Sequence 71633, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 71633
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-71633

Query Match 56.1%; Score 32; DB 5; Length 506;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 QLTPYIQR 11
| :||| |
Db 96 QQSPYIQR 103

RESULT 14

US-09-724-676A-71633
; Sequence 71633, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 71633
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-71633

Query Match 56.1%; Score 32; DB 5; Length 506;
Best Local Similarity 75.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 QLTPYIQR 11
| :||| |
Db 96 QQSPYIQR 103

RESULT 15

US-09-724-676-71621
; Sequence 71621, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28

; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 71621
; LENGTH: 537
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-71621

Query Match 56.1%; Score 32; DB 5; Length 537;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 QLTPYIQR 11
| :||| |
Db 96 QQSPYIQR 103

Search completed: January 7, 2003, 17:18:30
Job time : 25 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using SW model

Run on: January 7, 2003, 17:13:19 ; Search time 16 Seconds
(without alignments)
20.228 Million cell updates/sec

Title: US-09-623-006B-5
Perfect score: 57
Sequence: 1 MKRQLRYIQR 11

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep.*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep.*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep.*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep.*
5: /cgn2_6/prodata/1/1aa/CTUS_COMB.pep.*
6: /cgn2_6/prodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	66.7	641	1	US-07-718-535-3 Sequence 3, Appl1
2	38	66.7	641	1	US-08-161-999-3 Sequence 3, Appl1
3	36	63.2	284	2	US-08-424-641B-2 Sequence 2, Appl1
4	36	63.2	284	2	US-08-820-980-2 Sequence 2, Appl1
5	36	63.2	284	2	US-08-826-439-2 Sequence 2, Appl1
6	36	63.2	284	4	US-08-913-159-2 Sequence 2, Appl1
7	36	63.2	911	2	US-08-928-692-59 Sequence 59, Appl1
8	36	63.2	911	4	US-09-339-972-58 Sequence 59, Appl1
9	36	63.2	916	2	US-08-928-692-58 Sequence 58, Appl1
10	36	63.2	916	4	US-09-339-972-58 Sequence 58, Appl1
11	34	59.6	366	4	US-08-928-692-58 Sequence 28, Appl1
12	34	59.6	366	4	US-09-339-972-58 Sequence 28, Appl1
13	32	56.1	263	2	US-08-634-924B-2 Sequence 2, Appl1
14	32	56.1	391	4	US-09-134-001C-3952 Sequence 3952, Ap
15	32	56.1	2404	4	US-09-134-001C-3464 Sequence 3464, Ap
16	31	54.4	263	4	US-09-134-001C-4941 Sequence 4941, Ap
17	31	54.4	366	4	US-09-134-001C-5067 Sequence 5067, Ap
18	31	54.4	398	1	US-08-176-413-5 Sequence 5, Appl1
19	31	54.4	398	2	US-08-641-038A-2 Sequence 2, Appl1
20	31	54.4	398	2	US-09-059-178-2 Sequence 2, Appl1
21	31	54.4	398	2	US-08-642-541-2 Sequence 2, Appl1
22	31	54.4	398	4	US-09-260-889-2 Sequence 2, Appl1
23	31	54.4	398	4	US-09-347-878-12 Sequence 12, Appl1
24	31	54.4	398	4	US-09-347-878-14 Sequence 14, Appl1
25	31	54.4	398	4	US-09-479-275-7 Sequence 7, Appl1
26	31	54.4	398	5	PCT-US94-14919-5 Sequence 5, Appl1
27	31	54.4	399	4	US-09-494-921-2 Sequence 2, Appl1

28	31	54.4	488	6	5223391-9 Patent No. 5223391
29	31	54.4	503	4	US-08-740-223A-11 Sequence 11, Appl1
30	31	54.4	503	4	US-09-709-188-11 Sequence 11, Appl1
31	31	54.4	509	2	US-08-665-926-8 Sequence 8, Appl1
32	31	54.4	509	4	US-08-740-223A-10 Sequence 10, Appl1
33	31	54.4	509	4	US-09-202-491-2 Sequence 2, Appl1
34	31	54.4	509	4	US-09-202-491-3 Sequence 3, Appl1
35	31	54.4	509	4	US-09-709-188-10 Sequence 10, Appl1
36	31	54.4	516	1	US-08-356-340-4 Sequence 4, Appl1
37	31	54.4	516	2	US-08-786-555-4 Sequence 2, Appl1
38	31	54.4	525	1	US-08-356-340-2 Sequence 2, Appl1
39	31	54.4	525	2	US-08-786-555-2 Sequence 2, Appl1
40	31	54.4	612	2	US-08-673-789-11 Sequence 11, Appl1
41	31	54.4	620	3	US-09-126-646-2 Sequence 2, Appl1
42	31	54.4	620	4	US-09-421-491-2 Sequence 2, Appl1
43	31	54.4	662	2	US-09-016-000-5 Sequence 5, Appl1
44	31	54.4	824	1	US-08-221-750X-3 Sequence 3, Appl1
45	31	54.4	973	1	US-08-162-809-8 Sequence 8, Appl1

ALIGNMENTS

RESULT 1
US-07-718-535-3
Sequence 3, Application US/07718535
Patent No. 5322764
GENERAL INFORMATION:
APPLICANT: Salyers, Abigail A.,
APPLICANT: Shoemaker, Nadja B.,
APPLICANT: Nikolic, Mikelon P.
TITLE OF INVENTION: Method and Materials For
TITLE OF INVENTION: Introducing DNA Into Prevotella ruminicola
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: William Brinks Olds Hofer Gilson and Lioue
STREET: P.O. Box 10395
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60610
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM XT
OPERATING SYSTEM: MS-DOS 3.31
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07718,535
FILING DATE: 05-JUN-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Crook, Marnell M.
REGISTRATION NUMBER: 31,071
REFERENCE/DOCKET NUMBER: 3617/22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 321-4290
TELEFAX: (312) 321-4299
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 641 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
US-07-718-535-3

Query Match 66.7%; Score 38; DB 1; Length 641;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Cy 3 ROTRYPIQR 11
Db 518 RQITPIYVR 526

RESULT 2
US-08-161-999-3
; Sequence 3, Application US/08161999
; Patent No. 5674733
; GENERAL INFORMATION:
; APPLICANT: Salyers, Abigail A.,
; APPLICANT: Shoemaker, Nadja B.,
; APPLICANT: Nikolich, Mikelion P.,
; TITLE OF INVENTION: Method and Materials For
; TITLE OF INVENTION: Introducing DNA Into Prevotella ruminicola
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Willian Brinks Olds Hofer Gilson and Lione
; STREET: P.O. Box 10395
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM XT
; OPERATING SYSTEM: MS-DOS 3.31
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/161,999
; FILING DATE: 02-DEC-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/719,535
; FILING DATE: 05-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Crook, Wannell M.
; REGISTRATION NUMBER: 31,071
; REFERENCE/DOCKET NUMBER: 3617/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 321-4200
; TELEFAX: (312) 321-4299
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 641 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
US-08-161-999-3
Query Match 66.7%; Score 38; DB 1; Length 641;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 RLQTPVQIR 11
Db 518 RLQTPVQIR 526
RESULT 3
US-08-424-641B-2
; Sequence 2, Application US/08424641B
; Patent No. 5824523
; GENERAL INFORMATION:
; APPLICANT: Sylvain Moineau, Shirley A.,
; APPLICANT: Walker, Ebenezer R. Vedamuthu,
; APPLICANT: and Peter A. Vandenbergh
; TITLE OF INVENTION: Isolated DNA Encoding
; TITLE OF INVENTION: Enzyme For Phage
; TITLE OF INVENTION: Resistance
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ian C. McLeod
; STREET: 2190 Commons Parkway
; CITY: Okemos
; STATE: Michigan
; COUNTRY: USA

ZIP: 48864
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb
; MEDIUM TYPE: storage
; COMPUTER: Acer
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,641B
; FILING DATE: April 19, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/366,480
; FILING DATE: December 30, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ian C. McLeod
; REGISTRATION NUMBER: 20,931
; REFERENCE/DOCKET NUMBER: MT 4.1-151
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 347-4100
; TELEFAX: (517) 347-4103
; TELEEX: No. 5824523e
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 284 Amino Acids
; TYPE: Amino Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE: Peptide
US-08-424-641B-2
Query Match 63.2%; Score 36; DB 2; Length 284;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 KRQLTPYIQ 10
Db 21 KRQLPHIQ 29
RESULT 4
US-08-820-980-2
; Sequence 2, Application US/08820980
; Patent No. 5925388
; GENERAL INFORMATION:
; APPLICANT: Sylvain Moineau, Shirley A.,
; APPLICANT: Walker, Ebenezer R. Vedamuthu,
; APPLICANT: and Peter A. Vandenbergh
; TITLE OF INVENTION: Isolated DNA Encoding
; TITLE OF INVENTION: Enzyme For Phage
; TITLE OF INVENTION: Resistance
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ian C. McLeod
; STREET: 2190 Commons Parkway
; CITY: Okemos
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48864
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb
; MEDIUM TYPE: storage
; COMPUTER: Acer
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/820,980
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/424,641
; FILING DATE: April 19, 1995

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: Quest 4.1-156
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEFAX: (517) 347-4103
TELEX: No. 5925388e
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 284 Amino Acids
TYPE: Amino Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Peptide
US-08-820-980-2

Query Match 63.2%; Score 36; DB 2; Length 284;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KRQUTPYIQ 10
Db 21 KRQLPHIQ 29

RESULT 5
US-08-826-439-2
Sequence 2, Application US/08826439
Patent No. 5972673
GENERAL INFORMATION:
APPLICANT: Sylvain Moineau, Shirley A.
APPLICANT: Walker, Ebenezer R. Vedamuthu,
APPLICANT: and Peter A. Vandenberg
TITLE OF INVENTION: Isolated DNA Encoding
TITLE OF INVENTION: Enzyme For Phage
TITLE OF INVENTION: Resistance
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ian C. McLeod
STREET: 2190 Commons Parkway
CITY: Okemos
STATE: Michigan
COUNTRY: USA
ZIP: 48864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb
MEDIUM TYPE: Storage
COMPUTER: Acer
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/826,439
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,641
FILING DATE: April 19, 1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: Quest 4.1-155
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELEFAX: (517) 347-4103
TELEX: No. 5972673e
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 284 Amino Acids
TYPE: Amino Acid
STRANDEDNESS: Single

TOPOLOGY: Linear
MOLECULE TYPE: Peptide
US-08-826-439-2

Query Match 63.2%; Score 36; DB 2; Length 284;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KRQUTPYIQ 10
Db 21 KRQLPHIQ 29

RESULT 6

US-08-913-159-2
Sequence 2, Application US/08913159
Patent No. 6300109
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Plasmid-derived type II
TITLE OF INVENTION: restriction-modification systems from *Lactococcus lactis*
NUMBER OF SEQUENCES: 14
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,159
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 0179/95
FILING DATE: 17-FEB-1995
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 284 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-913-159-2

Query Match 63.2%; Score 36; DB 4; Length 284;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KRQUTPYIQ 10
Db 21 KRQLPHIQ 29

RESULT 7

US-08-928-692-59
Sequence 59, Application US/08928692
Patent No. 5958727
GENERAL INFORMATION:
APPLICANT: Brody, Howard
APPLICANT: Yaver, Deborah S.
APPLICANT: Lamsa, Michael
APPLICANT: Hansen, Kim
TITLE OF INVENTION: Methods for Modifying the Production of
TITLE OF INVENTION: a Polypeptide
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5958727e No. 5958727disk of No. 5958727th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,692
FILING DATE: 12-SEPT-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4944.200-US
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 911 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 5958727e
US-08-928-692-59

Query Match 63.2%; Score 36; DB 2; Length 911;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKRQLTPYI 9
Db 811 VKRALTPYV 819

RESULT 8
US-09-339-972-59
Sequence 59, Application US/09339972
Patent No. 6323002
GENERAL INFORMATION:
APPLICANT: Brody, Deborah S.
APPLICANT: Yaver, Deborah S.
APPLICANT: Lamsa, Michael
APPLICANT: Hansen, Kim
TITLE OF INVENTION: Methods for Modifying the Production of
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6323002o No. 6323002disk of No. 6323002th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/339,972
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/928,692
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4944.200-US
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 911 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: No. 6323002e
US-09-339-972-59

Query Match 63.2%; Score 36; DB 4; Length 911;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKRQLTPYI 9
Db 811 VKRALTPYV 819

RESULT 9
US-08-928-692-58
Sequence 58, Application US/08928692
Patent No. 5958727
GENERAL INFORMATION:
APPLICANT: Brody, Howard
APPLICANT: Yaver, Deborah S.
APPLICANT: Lamsa, Michael
APPLICANT: Hansen, Kim
TITLE OF INVENTION: Methods for Modifying the Production of
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5958727o No. 5958727disk of No. 5958727th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,692
FILING DATE: 12-SEPT-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4944.200-US
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 916 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 5958727e
US-08-928-692-58

Query Match 63.2%; Score 36; DB 2; Length 916;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKRQLTPYI 9
Db 816 VKRALTPYV 824

RESULT 10
US-09-339-972-58
Sequence 58, Application US/09339972
Patent No. 6323002
GENERAL INFORMATION:
APPLICANT: Brody, Howard
APPLICANT: Yaver, Deborah S.

APPLICANT: Lamsa, Michael
APPLICANT: Hansen, Kim
TITLE OF INVENTION: Methods for Modifying the Production of
TITLE OF INVENTION: a Polypeptide
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESS: No. 63230020 No. 6323002disk of No. 6323002th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/339,972
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/928,692
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4944.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 916 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6323002e
US-09-339-972-58
Query Match 63.2%; Score 36; DB 4; Length 916;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKROLTPYI 9
:|||||:
Db 816 VKRALTPYV 824
RESULT 11
US-08-928-692-28
Sequence 28, Application US/08928692
Patent No. 5958727
GENERAL INFORMATION:
APPLICANT: Brody, Howard
APPLICANT: Yaver, Deborah S.
APPLICANT: Lamsa, Michael
APPLICANT: Hansen, Kim
TITLE OF INVENTION: Methods for Modifying the Production of
TITLE OF INVENTION: a Polypeptide
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESS: No. 59587270 No. 5958727disk of No. 5958727th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,692
FILING DATE: 12-SEPT-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4944.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 366 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 5958727e
US-08-928-692-28
Query Match 59.6%; Score 34; DB 2; Length 366;
Best Local Similarity 85.7%; Pred. No. 40;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 5 LTPYIOR 11
:|||||:
Db 202 LTPYIER 208
RESULT 12
US-09-339-972-28
Sequence 28, Application US/09339972
Patent No. 6323002
GENERAL INFORMATION:
APPLICANT: Brody, Howard
APPLICANT: Yaver, Deborah S.
APPLICANT: Lamsa, Michael
APPLICANT: Hansen, Kim
TITLE OF INVENTION: Methods for Modifying the Production of
TITLE OF INVENTION: a Polypeptide
NUMBER OF SEQUENCES: 80
CORRESPONDENCE ADDRESS:
ADDRESS: No. 63230020 No. 6323002disk of No. 6323002th America, Inc.
STREET: 405 Lexington Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10174
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/339,972
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/928,692
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4944.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 366 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

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; MOLECULE TYPE: No. 6323002e
; US-09-339-972-28

Query Match      59.6%; Score 34; DB 4; Length 366;
Best Local Similarity 85.7%; Pred. No. 40;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 LTPYIOR 11
Db 202 LTPYIER 208
|||||:|

RESULT 13
US-08-634-924B-2
; Sequence 2, Application US/08634924B
; Patent No. 5834419
; GENERAL INFORMATION:
; APPLICANT: McFADDEN, GRANT
; APPLICANT: LUCAS, ALEXANDRA
; TITLE OF INVENTION: CHEMOKINE BINDING PROTEIN AND METHODS OF
; TITLE OF INVENTION: USE THEREFOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: California
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/634,924B
; FILING DATE: 19-APR-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/424,850
; FILING DATE: 19-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A.,
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: PD-3675
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 455-5100
; TELEFAX: (619) 455-5110
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-634-924B-2

Query Match      56.1%; Score 32; DB 2; Length 263;
Best Local Similarity 62.5%; Pred. No. 70;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KRQLTPIYI 9
Db 207 KREVSPYI 214
||||:|

RESULT 14
US-09-134-001C-3952
; Sequence 3952, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
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; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3952
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
; US-09-134-001C-3952

Query Match      56.1%; Score 32; DB 4; Length 391;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 KRQLTPIYIOR 11
Db 141 KRWITPYSQR 150
|||||

RESULT 15
US-09-134-001C-3464
; Sequence 3464, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3464
; LENGTH: 2404
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
; US-09-134-001C-3464

Query Match      56.1%; Score 32; DB 4; Length 2404;
Best Local Similarity 62.5%; Pred. No. 8.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 QLTPIYIOR 11
Db 154 QLTPIYIOR 161
||||:|

Search completed: January 7, 2003, 17:15:30
Job time : 18 secs
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PD 3/31/48 - PC
OK. - 3/25/49 (P⁴_{us-0})

Resect 4 WO Ref



OM protein - protein search, using SW model

41.879 Million cell updates/sec

Scoring table: BLOSUM62

Total number of hits satisfying chosen parameters: 908470

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database

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15	/SIDS2/gcgdata/geneseq/geneexp-emb1/A11994.DAT *
16	/SIDS2/gcgdata/geneseq/geneexp-emb1/A11995.DAT *
17	/SIDS2/gcgdata/geneseq/geneexp-emb1/A11996.DAT *
18	/SIDS2/gcgdata/geneseq/geneexp-emb1/A11997.DAT *
19	/SIDS2/gcgdata/geneseq/geneexp-emb1/A11998.DAT *
20	/SIDS2/gcgdata/geneseq/geneexp-emb1/A11999.DAT *
21	/SIDS2/gcgdata/geneseq/geneexp-emb1/A12000.DAT *
22	/SIDS2/gcgdata/geneseq/geneexp-emb1/A12001.DAT *
23	/SIDS2/gcgdata/geneseq/geneexp-emb1/A12002.DAT *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	57	100.0	11	20	AAV42557	Apoliipoprotein A-I
2	50	87.7	391	22	AAB90665	Human secreted pro
3	46	80.7	183	14	AAR39482	Human apolip
4	46	80.7	328	14	AAR39484	Human apolip
5	46	80.7	333	14	AAR39481	Human apolip
6	46	80.7	333	14	AAR39488	Human apolip
7	46	80.7	333	14	AAR39490	Human apolip
8	46	80.7	333	14	AAR39495	Human apolip
9	46	80.7	337	14	AAR39485	Human apolip
10	46	80.7	337	14	AAR39492	Human apolip

11	337	14	AAK394487	Human apolAIV muteI
12	342	14	AAK39467	Human apolAIV muteI
13	342	14	AAK39489	Human apolAIV muteI
14	342	14	AAK39491	Human apolAIV muteI
15	342	14	AAK39496	Human apolAIV muteI
16	346	14	AAK39493	Human apolAIV muteI
17	363	14	AAK39478	Human apolAIV muteI
18	363	14	AAK39479	Human apolAIV muteI
19	373	14	AAK39486	Human apolAIV muteI
20	377	14	AAK39443	Human apolIpoproteE
21	377	14	AAK39480	Human apolAIV muteI
22	377	14	AAK39499	Human apolAIV muteI
23	377	14	AAK39500	Human apolAIV muteI
24	377	14	AAK39502	Human apolAIV muteI
25	377	14	AAK39501	Human apolAIV muteI
26	377	14	AAK45242	Human apolAIV muteI
27	377	14	AAK45243	Human apolAIV muteI
28	377	14	AAK45244	Human apolAIV muteI
29	386	23	AAU10860	Human apolIpoproteE
30	386	23	AAU10861	Human apolIpoproteE
31	386	23	AAU10862	Human apolIpoproteE
32	396	23	AAU10863	Human apolIpoproteE
33	396	23	AAU10864	Human apolIpoproteE
34	396	23	AAU10865	Human apolIpoproteE
35	396	23	AAU10867	Human apolIpoproteE
36	396	23	AAU10868	Human apolIpoproteE
37	396	23	AAU10869	Human apolIpoproteE
38	396	23	AAU10865	Human apolIpoproteE
39	66	22	AAE09591	Human gene f encodE
40	66	22	AAU18371	Human endocrine poE
41	322	22	AAU18370	E. coli growth and
42	352	22	AAK98978	Human ORK protein
43	352	22	ABP08845	Human gene product d
44	122	23	ABP08845	Chlamydia pneumonia
45	157	13	AAK30089	
46	517	20	AAK34880	

ALIGNMENTS

RESULT 1
AAV42557

AA
AC
...
AAAY42557;

DE Apolipoprotein A-IV derived lipid oxidation suppressant peptide #5.

KW cholesterol; cardiovascular disease; heart disease; atherosclerosis
KW lipoprotein; angina; myocardial infarction; stroke; thrombosis;
KW antioxidant; hypolipidaemic; apolipoprotein.

OS Synthetic.

OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FM	modified	11

/note= "Optionally has a C-terminal amide

PN W09950286-A2.

PD 07-OCT-1999.

25-MAR-1999: 99W0-ITS06580

31-MAP-1999. 99TIC-0080131

XX
XX
XXXXXX

XX

XX:

DR WPI; 1999-580739/49.
 XX Treating conditions associated with lipid oxidation or preventing
 PT oxidation in lipid-containing food, lipid containing pharmaceuticals or
 PT cosmetic or dermatological compositions -
 XX Claim 4; Page 53; 73pp; English.
 PS This sequence represents a peptide (#5) derived from apolipoprotein
 XX (apo) A-IV with lipid oxidation inhibitory activity. Lipid oxidation
 CC plays a role in the development of atherosclerosis, a main cause of
 CC coronary heart disease. Atherosclerosis is thought to begin with local
 CC injury to the arterial endothelium, followed by proliferation of
 CC arterial smooth muscle cells, along with deposition of lipid and
 CC accumulation of foam cells in the lesion. As the atherosclerotic plaque
 CC develops, it progressively occludes more and more blood vessel and can
 CC eventually lead to ischaemia or infarction. Both the plasma concentration
 CC and qualitative characteristics of low density lipoproteins (LDL) are
 CC risk factors in atherogenesis. Oxidation causes important changes in the
 CC primary structure of the main LDL apolipoprotein, apolipoprotein B100
 CC (apo B-100). These changes, by helping LDL absorption by macrophages,
 CC causes the intracellular accumulation of esters of cholesterol and the
 CC formation of foam cells, with subsequent development of the
 CC atherosclerotic plaque. The apo A-IV derived peptides can be used for
 CC inhibiting lipid oxidation. The peptides can be used for treating
 CC conditions associated with lipid oxidation. For example, they can be used
 CC for treating or inhibiting the progression of atherosclerosis. They can
 CC also be used for preventing oxidation in lipid-containing foods,
 CC lipid-containing pharmaceuticals or cosmetic or dermatological
 CC compositions. As these peptides comprise specific portions of the native
 CC apo A-IV protein, there should be no immunogenicity problems with their
 CC administration to humans.

SQ Sequence 11 AA;

Query Match 100.0%; Score 57; DB 20; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.00019;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRQLTPYIQR 11
 |||||
 DB 1 MKRQLTPYIQR 11

RESULT 2
 AAB90665
 ID AAB90665 standard; Protein; 391 AA.

XX AAB90665;

XX 01-JUN-2001 (first entry)

XX Human secreted protein, SEQ ID NO: 208.

XX Human; secreted protein; immunomodulatory; antisclerotic;
 XX dermatological; antiinflammatory; anti-HIV; cytostatic; cardiant;
 XX vascular; anti-angiogenic; ophthalmological; neuroprotectant;
 XX neurotropic; anticonvulsant; antialzheimers; antiparkinsonian;
 XX antimicrobial; vulnery; vaccine; gene therapy; cancer;
 XX protein coordinate data; infection.

XX Homo sapiens.

XX WO200121658-A1.

XX 29-MAR-2001.

XX 22-SEP-2000; 2000WO-US26013.

XX 24-SEP-1999; 99US-0155709.

XX (HUMA-) HUMAN GENOME SCI INC.

XX

PI Ni J, Baker KP, Birse CE, Ebner R, Fiscella M, Komatsoulis GA;
 PI Lafleur DW, Moore PA, Olsen HS, Rosen CA, Ruben SA, Soppet DR;
 PI Young PE, Wei P, Florence KA;
 XX WPI; 2001-235311/24.
 XX Nucleic acids encoding 32 human secreted polypeptides, useful for
 PT preventing, diagnosing and/or treating e.g. cancers, Parkinson's
 PT disease and diabetic retinopathy -
 XX Disclosure; Page 871-872; 890pp; English.
 PS The present sequence is provided in a specification relating to nucleic
 CC acid molecules encoding 32 novel human secreted polypeptides. The nucleic
 CC acid molecules and polypeptides may be used in the prevention, diagnosis
 CC and treatment of diseases such as immune disorders (e.g. multiple
 CC sclerosis, systemic lupus erythematosus and human immuno-deficiency virus
 CC (HIV) infections), hyperproliferative disorders (e.g. cancers and
 CC Gaucher's disease), cardiovascular diseases (e.g. Scimitar syndrome,
 CC Chaga's cardiomyopathy and coronary arteriosclerosis), angiogenic
 CC disorders (e.g. corneal graft neovascularisation and diabetic
 CC retinopathy), neurological disorders (e.g. Huntington's chorea,
 CC Alzheimer's disease and Parkinson's disease), infectious diseases and/or
 CC for promoting wound healing, regeneration and/or chemotaxis. The nucleic
 CC acid molecules may be used to produce the secreted polypeptides. They may
 CC also be used as DNA probes in diagnostic assays to detect and quantitate
 CC the presence of similar nucleic acid sequences in samples. The
 CC polypeptides may be used as antigens in the production of antibodies and
 CC in assays to identify modulators of their expression and activity.

SQ Sequence 391 AA;

Query Match 87.7%; Score 50; DB 22; Length 391;
 Best Local Similarity 90.9%; Pred. No. 0.18;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRQLTPYIQR 11
 |||||
 DB 153 MKLQLTPYIQR 163

RESULT 3
 AAR39482

ID AAR39482 standard; Protein; 183 AA.

XX AAR39482;

XX 28-JAN-1994; (first entry)

XX Human apoAIV mutein P(deltaC194).

XX apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;
 XX coronary disease; chylomicron; cholesterol transport;
 XX plaque deposition; lecithin-cholesterol-acyltransferase; LCAT.

XX Synthetic.

XX Key Location/Qualifiers
 XX 2..183

XX Protein /label= P(deltaC194)

XX /note= "the 194 C-terminal amino acids of
 XX human apoAIV have been deleted"

XX WO9315198-A.

XX 05-AUG-1993.

XX 26-JAN-1993; 93WO-FR00073.

XX 27-JAN-1992; 92FR-0000806.

XX (RHON) RHONE POULENC RORER SA.

XX

PI Deneffe P, Guinet F, Latta M, Murry-Brelrier A;
 XX WPI; 1993-258676/32.
 DR
 XX
 PT New apolipoprotein AIV mutant polypeptide(s) - useful for drug
 PT design and/or treatment of hypercholesterolaemia
 XX
 PS Claim 7; Page 31-32 and Page 4; 42pp; French.
 XX
 CC Human apolipoprotein AIV is a major component of chylomicrons in
 CC lymph but is mainly found in the plasma in unassociated form. The
 CC apoAIV mediates inverse transport of cholesterol. The invention
 CC covers polypeptides which are derived from apoAIV by deletion of
 CC at least 10 terminal amino acids, by deletion of a helix or pair
 CC of helices, by addition of a heterologous polypeptide portion or
 CC by a point mutation. Such muteins are useful in the design of
 CC hypocholesterolaemic drugs to treat hypercholesterolaemia and
 CC atherosclerosis. AAR39482 is a specifically claimed mutein and the
 CC sequence has been compiled from the wild-type sequence (see AAR39443)
 CC and the description given in the disclosure; the mutant sequence is
 CC not shown in the specification.
 CC
 XX
 SQ Sequence 183 AA;
 Query Match 80.7%; Score 46; DB 14; Length 183;
 Best Local Similarity 72.7%; Pred. No. 0.5;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MKRQLTPYTOR 11
 Db 134 LRRQLTPYAQR 144
 RESULT 4
 AAR39484
 ID AAR39484 standard; Protein; 328 AA.
 XX
 AC AAR39484;
 XX
 DT 28-JAN-1994 (first entry)
 XX
 DE Human apoAIV mutein P(delta h1-2).
 XX
 KM apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;
 KM coronary disease; chylomicron; cholesterol transport;
 KM plaque deposition; lecithin-cholesterol-acyltransferase; LCAT.
 XX
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT Misc-difference 13..14
 FT /note= "helices 1-2 have been deleted from between
 FT these two sites"
 FT Region 14..46
 FT /note= "helix 3"
 FT Region 47..68
 FT /note= "helix 4"
 FT Region 69..90
 FT /note= "helix 5"
 FT Region 91..112
 FT /note= "helix 6"
 FT Region 113..134
 FT /note= "helix 7"
 FT Region 135..156
 FT /note= "helix 8"
 FT Region 157..178
 FT /note= "helix 9"
 FT Region 179..200
 FT /note= "helix 10"
 FT Region 201..218
 FT /note= "helix 11"
 FT Region 219..240
 FT /note= "helix 12"

FT Region 241..262
 FT /note= "helix 13"
 FT Region 263..284
 FT /note= "helix 14"
 FT Region 285..328
 FT /note= "helix 15"
 XX
 XX W09315198-A.
 XX
 PD 05-AUG-1993.
 XX
 PF 26-JAN-1993; 93MO-FR00073.
 XX
 PR 27-JAN-1992; 92PR-0000806.
 XX
 PA (RHON) RHONE POUJENC RORER SA.
 XX
 PI Deneffe P, Guinet F, Latta M, Murry-Brelrier A;
 XX WPI; 1993-258676/32.
 DR
 XX
 PT New apolipoprotein AIV mutant polypeptide(s) - useful for drug
 PT design and/or treatment of hypercholesterolaemia
 XX
 PS Claim 7; Page 31-32 and Page 4; 42pp; French.
 XX
 CC Human apolipoprotein AIV is a major component of chylomicrons in
 CC lymph but is mainly found in the plasma in unassociated form. The
 CC apoAIV mediates inverse transport of cholesterol. The invention
 CC covers polypeptides which are derived from apoAIV by deletion of
 CC at least 10 terminal amino acids, by deletion of a helix or pair
 CC of helices, by addition of a heterologous polypeptide portion or
 CC by a point mutation. Such muteins are useful in the design of
 CC hypocholesterolaemic drugs to treat hypercholesterolaemia and
 CC atherosclerosis. AAR39484 is a specifically claimed mutein and the
 CC sequence has been compiled from the wild-type sequence (see AAR39443)
 CC and the description given in the disclosure; the mutant sequence is
 CC not shown in the specification.
 CC
 XX
 SQ Sequence 328 AA;
 Query Match 80.7%; Score 46; DB 14; Length 328;
 Best Local Similarity 72.7%; Pred. No. 0.91;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MKRQLTPYTOR 11
 Db 85 LRRQLTPYAQR 95
 RESULT 5
 AAR39481
 ID AAR39481 standard; Protein; 333 AA.
 XX
 AC AAR39481;
 XX
 DT 28-JAN-1994 (first entry)
 XX
 DE Human apoAIV mutein P(delta C44).
 XX
 KM apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;
 KM coronary disease; chylomicron; cholesterol transport;
 KM plaque deposition; lecithin-cholesterol-acyltransferase; LCAT.
 XX
 OS Synthetic.
 XX
 PH Key Location/Qualifiers
 FT Protein 2..333
 FT /label= P(delta C44)
 FT /note= "the 44 C-terminal amino acids of
 FT human apoAIV have been deleted"
 PN W09315198-A.

XX PD 05-AUG-1993.
 XX XX
 PF 26-JAN-1993; 93WO-FR00073.
 XX XX
 PR 27-JAN-1992; 92FR-0000806.
 XX XX
 PA (RHON) RHONE POULENC RORER SA.
 XX XX
 XX Denefle P, Guinet F, Latta M, Murry-Brelrier A;
 XX WPI; 1993-258676/32.
 XX
 XX New apo:lipoprotein AIV mutant polypeptide(s) - useful for drug
 FT design and/or treatment of hypercholesterolaemia
 XX
 XX Claim 7; Page 31-32 and Page 4; 42pp; French.
 XX
 XX Human apolipoprotein AIV is a major component of chylomicrons in
 CC lymph but is mainly found in the plasma in unassociated form. The
 CC apoAIV mediates inverse transport of cholesterol. The invention
 CC covers polypeptides which are derived from apoAIV by deletion of
 CC at least 10 terminal amino acids, by deletion of a helix or pair
 CC of helices, by addition of a heterologous polypeptide portion or
 CC by a point mutation. Such muteins are useful in the design of
 CC hypocholesterolaemic drugs to treat hypercholesterolaemia and
 CC atherosclerosis. AAR39481 is a specifically claimed mutein and the
 CC sequence has been compiled from the wild-type sequence (see AAR39443)
 CC and the description given in the disclosure; the mutant sequence is
 CC not shown in the specification.
 XX
 XX SQ Sequence 333 AA;
 Query Match 80.7%; Score 46; DB 14; Length 333;
 Best Local Similarity 72.7%; Pred. No. 0.93;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MKRQLTPYIQR 11
 Db 134 LRRQLTPYQQR 144
 RESULT 6
 AAR39488
 ID AAR39488 standard; Protein; 333 AA.
 XX
 XX AAR39488;
 AC
 XX 28-JAN-1994 (first entry)
 XX
 XX Human apoAIV mutein P(delta h7-8).
 DE
 XX apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;
 KW coronary disease; chylomicron; cholesterol transport;
 KW plaque deposition; lecithin-cholesterol-acyltransferase; LCAT.
 XX
 XX Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Region 14..40
 FT /note= "helix 1"
 FT Region 41..62
 FT /note= "helix 2"
 FT Region 63..95
 FT /note= "helix 3"
 FT Region 96..117
 FT /note= "helix 4"
 FT Region 118..139
 FT /note= "helix 5"
 FT Region 140..161
 FT /note= "helix 6"
 FT Misc-difference 161..162
 FT /note= "helices 7-8 have been deleted from between

FT Region 162..183
 FT /note= "helix 9"
 FT Region 184..205
 FT /note= "helix 10"
 FT Region 206..223
 FT /note= "helix 11"
 FT Region 224..245
 FT /note= "helix 12"
 FT Region 246..267
 FT /note= "helix 13"
 FT Region 268..289
 FT /note= "helix 14"
 FT Region 290..333
 FT /note= "helix 15"
 XX
 XX WO9315198-A.
 XX
 XX 05-AUG-1993.
 XX
 XX 26-JAN-1993; 93WO-FR00073.
 XX
 XX 27-JAN-1992; 92FR-0000806.
 XX
 XX (RHON) RHONE POULENC RORER SA.
 XX
 XX Denefle P, Guinet F, Latta M, Murry-Brelrier A;
 XX WPI; 1993-258676/32.
 XX
 XX New apo:lipoprotein AIV mutant polypeptide(s) - useful for drug
 FT design and/or treatment of hypercholesterolaemia
 XX
 XX Claim 7; Page 31-32 and Page 4; 42pp; French.
 XX
 XX Human apolipoprotein AIV is a major component of chylomicrons in
 CC lymph but is mainly found in the plasma in unassociated form. The
 CC apoAIV mediates inverse transport of cholesterol. The invention
 CC covers polypeptides which are derived from apoAIV by deletion of
 CC at least 10 terminal amino acids, by deletion of a helix or pair
 CC of helices, by addition of a heterologous polypeptide portion or
 CC by a point mutation. Such muteins are useful in the design of
 CC hypocholesterolaemic drugs to treat hypercholesterolaemia and
 CC atherosclerosis. AAR39488 is a specifically claimed mutein and the
 CC sequence has been compiled from the wild-type sequence (see AAR39443)
 CC and the description given in the disclosure; the mutant sequence is
 CC not shown in the specification.
 XX
 XX SQ Sequence 333 AA;
 Query Match 80.7%; Score 46; DB 14; Length 333;
 Best Local Similarity 72.7%; Pred. No. 0.93;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MKRQLTPYIQR 11
 Db 134 LRRQLTPYQQR 144
 RESULT 7
 AAR39490
 ID AAR39490 standard; Protein; 333 AA.
 XX
 XX AAR39490;
 AC
 XX 28-JAN-1994 (first entry)
 XX
 XX Human apoAIV mutein P(delta h9-10).
 DE
 XX apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;
 KW coronary disease; chylomicron; cholesterol transport;
 KW plaque deposition; lecithin-cholesterol-acyltransferase; LCAT.
 XX

XX	Synthetic.
FH	Key
FT	Region
FT	Region
FT	Region
FT	Region
FT	Region
FT	Region
FT	Region
FT	Region
FT	Region
FT	Region
FT	Region
FT	Misc-difference
FT	/note= "helices 9-10 have been deleted from between these two sites"
FT	Region
FT	Region
FT	Region
FT	Region
FT	Region
FT	Region
FT	Region
PN	MO93I5198-A.
PD	05-AUG-1993.
PF	26-JAN-1993; 93WO-FR00073.
PR	27-JAN-1992; 92FR-00080806.
PR	(RHON) RHONE POULENC ROBER SA.
PA	
PI	Deneffe P, Guinet F, Latta M, Murry-Brelhier A;
DR	WPI; 1993-258676/32.
XX	
PT	New apo:Bipoprotein AIV mutant polypeptide(s) - useful for drug design and/or treatment of hypercholesterolaemia
PS	Claim 7, Page 31-32 and Page 5; 42pp; French.
CC	Human apolipoprotein AIV is a major component of chylomicrons in lymph but is mainly found in the plasma in unassociated form. The apoAIV mediates inverse transport of cholesterol. The invention covers polypeptides which are derived from apoAIV by deletion of at least 10 terminal amino acids, by detection of a helix or pair of helices, by addition of a heterologous polypeptide portion or by a point mutation. Such mutants are useful in the design of hypercholesterolaemic drugs to treat hypercholesterolaemia and atherosclerosis. AAR39490 is a specifically claimed mutein and the sequence has been compiled from the wild-type sequence (see AAR39443) and the description given in the disclosure; the mutant sequence is not shown in the specification.
XX	
XX	Sequence 333 AA;
XX	
XX	Query Match 80.7%; Score 46; DB 14; Length 333; Best Local Similarity 72.7%; Pred. No. 0.93; Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0. :: 1 MKKQLTPYIR 11

DB	134	LRRLTPYAQR	144
XX	XX	RESULT 8	
XX	XX	AAK39495	
XX	ID	AAK39495 standard; Protein; 333 AA.	
XX	AC	AAK39495;	
XX	DT	28-JAN-1994 (first entry)	
XX	DE	Human apoAIV mutcin P(delta h13-14).	
XX	KW	apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;	
XX	KM	coronary disease; chylomicron; cholesterol transport;	
XX	KW	plaque deposition; lecithin-cholesterol-acyltransferase, LCAT.	
XX	OS	Synthetic.	
XX	PH	Key	Location/Qualifiers
XX	FT	Region	14..40
XX	FT		/note="helix 1"
XX	FT	Region	41..62
XX	FT		/note="helix 2"
XX	FT	Region	63..95
XX	FT		/note="helix 3"
XX	FT	Region	96..117
XX	FT		/note="helix 4"
XX	FT	Region	118..139
XX	FT		/note="helix 5"
XX	FT	Region	140..161
XX	FT		/note="helix 6"
XX	FT	Region	162..183
XX	FT		/note="helix 7"
XX	FT	Region	184..205
XX	FT		/note="helix 8"
XX	FT	Region	206..227
XX	FT		/note="helix 9"
XX	FT	Region	228..249
XX	FT		/note="helix 10"
XX	FT	Region	250..267
XX	FT		/note="helix 11"
XX	FT	Region	268..289
XX	FT		/note="helix 12"
XX	FT	Misc-difference	289..290
XX	FT		/note="helices 13-14 have been deleted from between
XX	FT		these two sites"
XX	FT	Region	290..333
XX	FT		/note="helix 15"
XX	PN	WO9315198-A.	
XX	PD	05-AUG-1993.	
XX	XX	26-JAN-1993; 93WO-FR00073.	
XX	XX	27-JAN-1992; 92FR-0000806.	
XX	PA	(RHOE) RHOE POULENC RORER SA.	
XX	PI	Denefle P, Guinet F, Latta M, Murry-Breiller A;	
XX	XX	WPI, 1993-258676/32.	
XX	XX	New apo:lipoprotein AIV mutant polypeptide(s) - useful for drug	
XX	XX	design and/or treatment of hypercholesterolaemia	
XX	XX	Claim 7; Page 31-32 and Page 5; 42pp; French.	
XX	XX	Human apolipoprotein AIV is a major component of chylomicrons in	
XX	XX	lymph but is mainly found in the plasma in unassociated form. The	
XX	XX	apoAIV mediates inverse transport of cholesterol. The invention	
XX	XX	covers polypeptides which are derived from apoAIV by deletion of	

CC at least 10 terminal amino acids, by deletion of a helix or pair
CC of helices, by addition of a heterologous polypeptide portion or
CC by a point mutation. Such mutants are useful in the design of
CC hypocholesterolaemic drugs to treat hypercholesterolaemia and
CC atherosclerosis. AAR39495 is a specifically claimed mutein and the
CC sequence has been compiled from the wild-type sequence (see AAR39443)
CC and the description given in the disclosure; the mutant sequence is
CC not shown in the specification.
XX
SQ Sequence 333 AA;

Query Match 80.7%; Score 46; DB 14; Length 333;
Best Local Similarity 72.7%; Pred. No. 0.93;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRQLTPYIQR 11
Db 134 LRRQLTFYQQR 144

RESULT 9
AAR39485
ID AAR39485 standard; Protein; 337 AA.

AC AAR39485;

DT 28-JAN-1994 (first entry)

DE Human apoAIV mutein P(tag-delta h1-2).

KW apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;
KW coronary disease; chylomicron; cholesterol transport;
KW plaque deposition; lecithin-cholesterol-acyltransferase; LCAT;
KW tag purification marker.

OS Synthetic.

FH Key Location/Qualifiers

FT Peptide 1..10
FT /label= tag decapeptide
FT /note= "allows rapid, single stage purification
FT without affecting the properties of the
FT mature mutein"

FT Misc-difference 22..23
FT /note= "helices 1-2 have been deleted from between
FT these two sites"

FT Region 23..55

FT /note= "helix 3"

FT Region 56..77

FT /note= "helix 4"

FT Region 78..99

FT /note= "helix 5"

FT Region 100..121

FT /note= "helix 6"

FT Region 122..143

FT /note= "helix 7"

FT Region 135..165

FT /note= "helix 8"

FT Region 166..187

FT /note= "helix 9"

FT Region 188..209

FT /note= "helix 10"

FT Region 210..227

FT /note= "helix 11"

FT Region 228..249

FT /note= "helix 12"

FT Region 250..271

FT /note= "helix 13"

FT Region 272..293

FT /note= "helix 14"

FT Region 294..337

FT /note= "helix 15"

XX

PN WO9315198-A.
XX 05-AUG-1993.
XX 26-JAN-1993; 93WO-FR000073.
XX 27-JAN-1992; 92FR-0000806.
XX (RHON) RHONE POULENC RORER SA.
XX Denefle P, Guinet F, Latta M, Murry-Brellier A;
XX WPI; 1993-258676/32.
XX New apolipoprotein AIV mutant polypeptide(s) - useful for drug
XX design and/or treatment of hypercholesterolaemia
XX Claim 7; Page 31-32 and Page 4; 42pp; French.
XX Human apolipoprotein AIV is a major component of chylomicrons in
XX lymph but is mainly found in the plasma in unassociated form. The
XX apoAIV mediates inverse transport of cholesterol. The invention
XX covers polypeptides which are derived from apoAIV by deletion of
XX at least 10 terminal amino acids, by deletion of a helix or pair
XX of helices, by addition of a heterologous polypeptide portion or
XX by a point mutation. Such mutants are useful in the design of
XX hypocholesterolaemic drugs to treat hypercholesterolaemia and
XX atherosclerosis. AAR39485 is a specifically claimed mutein and the
XX sequence has been compiled from the wild-type sequence (see AAR39443)
XX and the description given in the disclosure; the mutant sequence is
XX not shown in the specification.
SQ Sequence 337 AA;

Query Match 80.7%; Score 46; DB 14; Length 337;
Best Local Similarity 72.7%; Pred. No. 0.94;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKRQLTPYIQR 11
Db 94 LRRQLTFYQQR 104

RESULT 10
AAR39492
ID AAR39492 standard; Protein; 337 AA.

AC AAR39492;

DT 28-JAN-1994 (first entry)

DE Human apoAIV mutein P(delta h11-12).

KW apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;
KW coronary disease; chylomicron; cholesterol transport;
KW plaque deposition; lecithin-cholesterol-acyltransferase; LCAT.

OS Synthetic.

FH Key Location/Qualifiers

FT Region 14..40

FT /note= "helix 1"

FT Region 41..62

FT /note= "helix 2"

FT Region 63..95

FT /note= "helix 3"

FT Region 96..117

FT /note= "helix 4"

FT Region 118..139

FT /note= "helix 5"

FT Region 140..161

FT /note= "helix 6"

FT Region 162..183

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FT      /note= "helix 7"
FT      Region
FT      184..205
FT      /note= "helix 8"
FT      Region
FT      206..227
FT      /note= "helix 9"
FT      Region
FT      228..249
FT      /note= "helix 10"
FT      Misc-difference
FT      249..250
FT      /note= "helices 11-12 have been deleted from between
FT      these two sites"
FT      Region
FT      250..271
FT      /note= "helix 13"
FT      Region
FT      272..293
FT      /note= "helix 14"
FT      Region
FT      294..337
FT      /note= "helix 15"
XX
XX      WO9315198-A.
XX      05-AUG-1993.
XX
XX      26-JAN-1993; 93WO-FR00073.
XX
XX      27-JAN-1992; 92FR-0000806.
XX
XX      (RHON ) RHONE POUTLENC RORER SA.
XX
XX      Deneffe P, Guinet F, Latta M, Murry-Breiller A;
XX      WPI; 1993-258676/32.
XX
XX      New apo:lipoprotein AIV mutant polypeptide(s) - useful for drug
XX      design and/or treatment of hypercholesterolaemia
XX
XX      Claim 7; Page 31-32 and Page 5; 42pp; French.
XX
XX      Human apolipoprotein AIV is a major component of chylomicrons in
XX      lymph but is mainly found in the plasma in unassociated form. The
XX      apoAIV mediates inverse transport of cholesterol. The invention
XX      covers polypeptides which are derived from apoAIV by deletion of
XX      at least 10 terminal amino acids, by deletion of a helix or pair
XX      of helices, by addition of a heterologous polypeptide portion or
XX      by a point mutation. Such muteins are useful in the design of
XX      hypocholesterolemic drugs to treat hypercholesterolaemia and
XX      atherosclerosis. AAR39492 is a specifically claimed mutein and the
XX      sequence has been compiled from the wild-type sequence (see AAR39443)
XX      and the description given in the disclosure; the mutant sequence is
XX      not shown in the specification.
XX
XX      Sequence 337 AA;
XX
XX      Query Match 80.7%; Score 46; DB 14; Length 337;
XX      Best Local Similarity 72.7%; Pred. No. 0.94;
XX      Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
XX      1 MKROLTPYIOR 11
XX      :|||||
XX      134 LRRQLTPYQIR 144
XX
XX      RESULT 11
XX      ID AAR39494
XX      AAR39494 standard; Protein; 337 AA.
XX
XX      AAR39494;
XX
XX      28-JAN-1994 (first entry)
XX
XX      Human apoAIV mutein P(delta h11-12, L87M).
XX
XX      apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;
XX      coronary disease; chylomicron; cholesterol transport;
XX      plaque deposition; lecithin-cholesterol acyltransferase; LCAT.
XX

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XX      Synthetic.
XX
XX      OS
XX      Key
XX      Protein
XX      Location/Qualifiers
XX      2..337
XX      /label= "(delta h11-12, L87M)
XX      /note= "helices 11-12 have been deleted from
XX      mature human apoAIV and wild-type Leu87
XX      has been substid. by Met"
XX
XX      Region
XX      14..40
XX      /note= "helix 1"
XX      Region
XX      41..62
XX      /note= "helix 2"
XX      Region
XX      63..95
XX      /note= "helix 3"
XX      Misc-difference
XX      87
XX      /note= "L87M"
XX      Region
XX      96..117
XX      /note= "helix 4"
XX      Region
XX      118..139
XX      /note= "helix 5"
XX      Region
XX      140..161
XX      /note= "helix 6"
XX      Region
XX      162..183
XX      /note= "helix 7"
XX      Region
XX      184..205
XX      /note= "helix 8"
XX      Region
XX      206..227
XX      /note= "helix 9"
XX      Region
XX      228..249
XX      /note= "helix 10"
XX      Misc-difference
XX      249..250
XX      /note= "helices 11-12 have been deleted from between
XX      these two sites"
XX
XX      Region
XX      250..271
XX      /note= "helix 13"
XX      Region
XX      272..293
XX      /note= "helix 14"
XX      Region
XX      294..337
XX      /note= "helix 15"
XX
XX      WO9315198-A.
XX      05-AUG-1993.
XX
XX      26-JAN-1993; 93WO-FR00073.
XX
XX      27-JAN-1992; 92FR-0000806.
XX
XX      (RHON ) RHONE POUTLENC RORER SA.
XX
XX      Deneffe P, Guinet F, Latta M, Murry-Breiller A;
XX      WPI; 1993-258676/32.
XX
XX      New apo:lipoprotein AIV mutant polypeptide(s) - useful for drug
XX      design and/or treatment of hypercholesterolaemia
XX
XX      Claim 7; Page 31-32 and Page 5; 42pp; French.
XX
XX      Human apolipoprotein AIV is a major component of chylomicrons in
XX      lymph but is mainly found in the plasma in unassociated form. The
XX      apoAIV mediates inverse transport of cholesterol. The invention
XX      covers polypeptides which are derived from apoAIV by deletion of
XX      at least 10 terminal amino acids, by deletion of a helix or pair
XX      of helices, by addition of a heterologous polypeptide portion or
XX      by a point mutation. Such muteins are useful in the design of
XX      hypocholesterolemic drugs to treat hypercholesterolaemia and
XX      atherosclerosis. AAR39494 is a specifically claimed mutein and the
XX      sequence has been compiled from the wild-type sequence (see AAR39443)
XX      and the description given in the disclosure; the mutant sequence is
XX      not shown in the specification.
XX

```

SQ Sequence 337 AA;
Query Match 80.7%; Score 46; DB 14; Length 337;
Best Local Similarity 72.7%; Pred. No. 0.94;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKRQLTPYIQR 11
:|||||
Db 134 LRQLTPYQQR 144

RESULT 12
AAR39487
ID AAR39487 standard; Protein; 342 AA.
XX
AC AAR39487;
XX
DT 28-JAN-1994 (first entry)
XX
DE Human apoAIV mutain P(tag-deltaC44).
XX
KW apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;
XX coronary disease; chylomicron; cholesterol transport;
KW plaque deposition; lecithin-cholesterol-acyltransferase; LCAT;
KW tag purification marker.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..10
FT /label= tag decapetide
FT /note= "allows rapid, single stage purification
FT without affecting the properties of the
FT mature mutain"
FT Protein 11..342
FT /label= P(deltaC44)
FT /note= "the 44 C-terminal amino acids of
FT mature human apoAIV have been deleted"

WO9315198-A.
XX
PD 05-AUG-1993.
XX
PF 26-JAN-1993; 93WO-FR000073.
XX
PR 27-JAN-1992; 92FR-0000806.
XX
PA (RHON) RHONE POULENC RORER SA.
XX
PI Denefle P, Guinet F, Latta M, Murry-Brelrier A;
XX
XX WPI; 1993-258676/32.
XX
XX New apo.lipoprotein AIV mutant polypeptide(s) - useful for drug
XX design and/or treatment of hypercholesterolaemia
XX
XX Claim 7; Page 31-32 and Page 4; 42pp; French.
XX
XX Human apolipoprotein AIV is a major component of chylomicrons in
XX lymph but is mainly found in the plasma in unassociated form. The
XX apoAIV mediates inverse transport of cholesterol. The invention of
XX covers polypeptides which are derived from apoAIV by deletion of
XX at least 10 terminal amino acids, by deletion of a helix or pair
XX of helices, by addition of a heterologous polypeptide portion or
XX by a point mutation. Such mutains are useful in the design of
XX hypocholesterolaemic drugs to treat hypercholesterolaemia and
XX atherosclerosis. AAR39487 is a specifically claimed mutain and the
XX sequence has been compiled from the wild-type sequence (see AAR39443)
XX and the description given in the disclosure, the mutant sequence is
XX not shown in the specification.

SQ Sequence 342 AA;

Query Match 80.7%; Score 46; DB 14; Length 342;
Best Local Similarity 72.7%; Pred. No. 0.95;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKRQLTPYIQR 11
:|||||
Db 143 LRQLTPYQQR 153

RESULT 13
AAR39489
ID AAR39489 standard; Protein; 342 AA.
XX
AC AAR39489;
XX
DT 28-JAN-1994 (first entry)
XX
DE Human apoAIV mutain P(tag-delta h7-8).
XX
KW apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;
XX coronary disease; chylomicron; cholesterol transport;
KW plaque deposition; lecithin-cholesterol-acyltransferase; LCAT;
KW tag purification marker.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..10
FT /label= tag decapetide
FT /note= "allows rapid, single stage purification
FT without affecting the properties of the
FT mature mutain"
FT Region 23..49
FT /note= "helix 1"
FT Region 50..71
FT /note= "helix 2"
FT Region 72..104
FT /note= "helix 3"
FT Region 105..126
FT /note= "helix 4"
FT Region 127..148
FT /note= "helix 5"
FT Region 149..170
FT /note= "helix 6"
FT Misc-difference 170..171
FT /note= "helices 7-8 have been deleted from between
FT these two sites"
FT Region 171..192
FT /note= "helix 9"
FT Region 193..214
FT /note= "helix 10"
FT Region 215..232
FT /note= "helix 11"
FT Region 233..254
FT /note= "helix 12"
FT Region 255..276
FT /note= "helix 13"
FT Region 277..298
FT /note= "helix 14"
FT Region 299..342
FT /note= "helix 15"
XX
XX WO9315198-A.
XX
XX 05-AUG-1993.
XX
XX 26-JAN-1993; 93WO-FR000073.
XX
XX 27-JAN-1992; 92FR-0000806.
XX
XX (RHON) RHONE POULENC RORER SA.
XX
XX Denefle P, Guinet F, Latta M, Murry-Brelrier A;
XX
XX WPI; 1993-258676/32.
XX
XX New apo.lipoprotein AIV mutant polypeptide(s) - useful for drug
XX design and/or treatment of hypercholesterolaemia
XX
XX Claim 7; Page 31-32 and Page 4; 42pp; French.
XX
XX Human apolipoprotein AIV is a major component of chylomicrons in
XX lymph but is mainly found in the plasma in unassociated form. The
XX apoAIV mediates inverse transport of cholesterol. The invention of
XX covers polypeptides which are derived from apoAIV by deletion of
XX at least 10 terminal amino acids, by deletion of a helix or pair
XX of helices, by addition of a heterologous polypeptide portion or
XX by a point mutation. Such mutains are useful in the design of
XX hypocholesterolaemic drugs to treat hypercholesterolaemia and
XX atherosclerosis. AAR39487 is a specifically claimed mutain and the
XX sequence has been compiled from the wild-type sequence (see AAR39443)
XX and the description given in the disclosure, the mutant sequence is
XX not shown in the specification.

SQ Sequence 342 AA;

XX DR WPI; 1993-258676/32.

XX PT New apo.lipoprotein AIV mutant polypeptide(s) - useful for drug

XX PT design and/or treatment of hypercholesterolaemia

XX PS Claim 7; Page 31-32 and Page 4; 42pp; French.

XX CC Human apolipoprotein AIV is a major component of chylomicrons in

XX CC lymph but is mainly found in the plasma in unassociated form. The

XX CC apoAIV mediates inverse transport of cholesterol. The invention of

XX CC covers polypeptides which are derived from apoAIV by deletion of

XX CC at least 10 terminal amino acids; by deletion of a helix or pair

XX CC of helices; by addition of a heterologous polypeptide portion or

XX CC by a point mutation. Such mutants are useful in the design of

XX CC hypocholesterolaemic drugs to treat hypercholesterolaemia and

XX CC atherosclerosis. AAR39489 is a specifically claimed mutuin and the

XX CC sequence has been compiled from the wild-type sequence (see AAR39443)

XX CC and the description given in the disclosure; the mutant sequence is

XX CC not shown in the specification.

XX SQ Sequence 342 AA;

Query Match 80.7%; Score 46; DB 14; Length 342;

Best Local Similarity 72.7%; Pred. No. 0.95;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKROLTPYIOR 11

DB 143 LRROLTPYAKR 153

RESULT 14

AAR39491

ID AAR39491 standard; Protein; 342 AA.

XX AC AAR39491;

XX DT 28-JAN-1994 (first entry)

XX DE Human apoAIV mutuin P(tag-delta h9-10).

XX KW apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;

KM coronary disease; chylomicron; cholesterol transport;

KM plaque deposition; lecithin-cholesterol-acyltransferase; LCAT;

KM tag purification marker.

XX OS Synthetic.

XX FH Key

FT Peptide

FT 1..10 Location/Qualifiers

FT /label= tag decapeptide

FT /note= "allows rapid, single stage purification

FT without affecting the properties of the

FT mature mutuin"

FT FT 23..49

FT /note= "helix 1"

FT FT 50..71

FT /note= "helix 2"

FT FT 72..104

FT /note= "helix 3"

FT FT 105..126

FT /note= "helix 4"

FT FT 127..148

FT /note= "helix 5"

FT FT 149..170

FT /note= "helix 6"

FT FT 171..192

FT /note= "helix 7"

FT FT 193..214

FT /note= "helix 8"

FT FT Misc-difference 214..215

FT /note= "helices 9-10 have been deleted from between

FT FT Region 215..232 these two sites"

FT FT /note= "helix 11"

FT FT 233..254

FT FT /note= "helix 12"

FT FT 255..276

FT FT /note= "helix 13"

FT FT 277..298

FT FT /note= "helix 14"

FT FT 299..342

FT FT /note= "helix 15"

XX PN WO9315198-A.

XX PD 05-AUG-1993.

XX PF 26-JAN-1993; 93MO-PR00073.

XX PR 27-JAN-1992; 92FR-0000806.

XX PA (RHON) RHONE POULENC RORER SA.

XX PI Denefle P, Guinet F, Latta M, Murry-Brelhier A;

XX DR WPI; 1993-258676/32.

XX PT New apo.lipoprotein AIV mutant polypeptide(s) - useful for drug

XX PT design and/or treatment of hypercholesterolaemia

XX PS Claim 7; Page 31-32 and Page 5; 42pp; French.

XX CC Human apolipoprotein AIV is a major component of chylomicrons in

XX CC lymph but is mainly found in the plasma in unassociated form. The

XX CC apoAIV mediates inverse transport of cholesterol. The invention of

XX CC covers polypeptides which are derived from apoAIV by deletion of

XX CC at least 10 terminal amino acids; by deletion of a helix or pair

XX CC of helices; by addition of a heterologous polypeptide portion or

XX CC by a point mutation. Such mutants are useful in the design of

XX CC hypocholesterolaemic drugs to treat hypercholesterolaemia and

XX CC atherosclerosis. AAR39491 is a specifically claimed mutuin and the

XX CC sequence has been compiled from the wild-type sequence (see AAR39443)

XX CC and the description given in the disclosure; the mutant sequence is

XX CC not shown in the specification.

XX SQ Sequence 342 AA;

Query Match 80.7%; Score 46; DB 14; Length 342;

Best Local Similarity 72.7%; Pred. No. 0.95;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKROLTPYIOR 11

DB 143 LRROLTPYAKR 153

RESULT 15

AAR39496

ID AAR39496 standard; Protein; 342 AA.

XX AC AAR39496;

XX DT 28-JAN-1994 (first entry)

XX DE Human apoAIV mutuin P(tag-delta h13-14).

XX KW apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;

KM coronary disease; chylomicron; cholesterol transport;

KM plaque deposition; lecithin-cholesterol-acyltransferase; LCAT;

KM tag purification marker.

XX OS Synthetic.

XX FH Key

FT Location/Qualifiers

FT Peptide 1..10
FT /label= tag_decapeptide
FT /note= "allows rapid, single stage purification
FT without affecting the properties of the
FT mature mutein"
FT
FT Region 23..49
FT /note= "helix 1"
FT Region 50..71
FT /note= "helix 2"
FT Region 72..104
FT /note= "helix 3"
FT Region 105..126
FT /note= "helix 4"
FT Region 127..148
FT /note= "helix 5"
FT Region 149..170
FT /note= "helix 6"
FT Region 171..192
FT /note= "helix 7"
FT Region 193..214
FT /note= "helix 8"
FT Region 215..236
FT /note= "helix 9"
FT Region 237..258
FT /note= "helix 10"
FT Region 259..276
FT /note= "helix 11"
FT Region 277..298
FT /note= "helix 12"
FT Misc-difference 298..299
FT /note= "helices 13-14 have been deleted from between
FT these two sites"
FT Region 299..342
FT /note= "helix 15"
FT
XX WO9315198-A.
XX
XX
XX 05-AUG-1993.
XX
XX 26-JAN-1993; 93WO-FR00073.
XX
XX 27-JAN-1992; 92FR-000806.
XX
XX (RHON) RHONE POULENC RORER SA.
XX
XX Denefle P, Guinet F, Latta M, Murry-Brelier A;
XX WPI; 1993-258676/32.
XX
XX New apolipoprotein AIV mutant polypeptide(s) - useful for drug
XX design and/or treatment of hypercholesterolaemia
XX
XX Claim 7; Page 31-32 and Page 5; 42pp; French.
XX
XX Human apolipoprotein AIV is a major component of chylomicrons in
XX lymph but is mainly found in the plasma in unassociated form. The
XX apoAIV mediates inverse transport of cholesterol. The invention
XX covers polypeptides which are derived from apoAIV by deletion of
XX at least 10 terminal amino acids, by deletion of a helix or pair
XX of helices, by addition of a heterologous polypeptide portion or
XX by a point mutation. Such muteins are useful in the design of
XX hypocholesterolaemic drugs to treat hypercholesterolaemia and
XX atherosclerosis. AAR39496 is a specifically claimed mutein and the
XX sequence has been compiled from the wild-type sequence (see AAR39443)
XX and the description given in the disclosure; the mutant sequence is
XX not shown in the specification.
XX
SQ Sequence 342 AA;

Query Match 80.7%; Score 46; DB 14; Length 342;
Best Local Similarity 72.7%; Pred. No. 0.95;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKRQLTPYIQR 11
Db 143 LRRQLTPYIQR 153
Search completed: January 7, 2003, 17:14:00
Job time : 49 secs